O'Bryen, Barbara

From:

Swope, Sheridan

Sent:

Monday, July 14, 2003 2:07 PM

To: Subject: O'Bryen, Barbara FW: 09966880

Importance:

High

Barb, May I get a copy of the search results for 09966880?

THANKS!

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes sheridan.swope@uspto.gov 703-305-1696 (voice) 703-308-3014 (FAX)

703-308-3014 (FAX) Mailbox: CM1 Rm10D01 Office: CM1 Rm12D12

----Original Message----

From:

STIC-Biotech/ChemLib

Sent:

Monday, July 14, 2003 1:45 PM

To: Subject: Swope, Sheridan RE: 09966880

Please check your mail box or call Barb O'Bryen. She completed the search on 7/8/03

----Original Message----

From:

Swope, Sheridan

Sent:

Monday, July 14, 2003 1:38 PM

To:

STIC-Biotech/ChemLib

Subject:

FW: 09966880

WHAT IS THE STATUS OF THIS RUSH REQUEST?

-----Original Message-----

From:

Swope, Sheridan

Sent:

Friday, July 04, 2003 2:26 PM

To:

STIC-Biotech/ChemLib

Subject:

FW: 09966880

-----Original Message-----

From:

Richter, Johann

Sent: To: Friday, July 04, 2003 2:06 PM

Cc:

Swope, Sheridan; STIC-Biotech/ChemLib Chan, Christina

Subject:

RE: 09966880

Approved.

Johann R. Richter, Ph.D., Esq.

Supervisory Patent Examiner

Biotechnology and Organic Chemistry

Art Unit 1621

703-308-4532

----Original Message----

From:

Swope, Sheridan

Sent:

Friday, July 04, 2003 1:59 PM

To: STIC-Biotech/ChemLib

Cc: Chan, Christina; Richter, Johann

Subject: 09966880 Importance: Hig

I made a mistake on the original request for this search. May I have this rushed?

For 09966880, pls search:

SID 7 oligo against the NT and AA data bases.

SID 8 oligo against the NT and AA data bases.

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes sheridan.swope@uspto.gov 703-305-1696 (voice) 703-308-3014 (FAX) Mailbox: CM1 Rm10D01 Office: CM1 Rm12D12

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ALIGNMENTS

RESULT 1 AAB24198

AAB24198 standard; Protein; 198 ₿

AAB24198;

05-FEB-2001 (first entry)

Human activation-induced cytidine deaminase SEQ ID NO:8

immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HTV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Discorge disease; ADDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; Activation-induced cytidine deaminase; AID; cytidine deaminase;

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                                                                TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCCTGCTACCGCGTCACCTGG
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                                                                                                          14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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2000US-0215135
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2000US-0224518
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2000US-0220963
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2000US-0217487
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2000US-0205515
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18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 30-AUG-2000;

2000US-0225758. 2000US-0225759. 2000US-02256279. 2000US-0226681. 2000US-02276868. 2000US-02271868. 2000US-022718. 2000US-022719. 2000US-022719.

-2000; -2000; -2000;

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Alignment Scores: Pred. No.:
               Score:
 Percent Similarity:
                                                                                                AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and cancers and treat immune/haematopoietic derived cells. AAK64703 cancers and cancer metastases of haematopoietic entigen genomic sequences from the present invention. AAK54942 to AAK94950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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11-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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N-PSDB; AAK61819.
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                                                                         Sequence
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2000US-0251989.
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2000US-0254097.
2001US-0259678.
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2000US-0249216
2000US-0249218
2000US-0249244
2000US-0249244
2000US-0249265
2000US-0249265
2000US-0249269
2000US-0249299
2000US-0249299
2000US-0249299
2000US-0250160
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2000US-0249207.
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 Length:
Matches:
Conservative:
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2000US-0234997. 2000US-0234998. 2000US-0235484.

2000US-0235834

2000US-0233065. 2000US-0234223. 2000US-0234274.

2000US-0232400. 2000US-0232401. 2000US-0233063. 2000US-0233064.

2000US-0232398 2000US-0232399 2000US-0231968 2000US-0232397

2000US-0235836. 2000US-0236327. 2000US-0236368. 2000US-0236369. 2000US-0236369. 2000US-0236370.

21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
02-CCT-2000
03-CCT-2000
03-CCT

2000US-0240960. 2000US-0241221. 2000US-0241785. 2000US-0241786. 2000US-0241787.

2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

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2000US-0236802. 2000US-0237037. 2000US-0237038. 2000US-0237039. 2000US-0237039. 2000US-0239935. 2000US-0239937.

2000US-0246475 2000US-0246475 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246524 2000US-0246524 2000US-0246525 2000US-0246526 2000US-0246527 2000US-0246527 2000US-0246527 2000US-0246532 2000US-0246532

01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0229287 2000US-0229343 2000US-0229344 2000US-0229345 2000US-0229509 2000US-0229513 2000US-0230437 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231244 2000US-0231413 2000US-0231414 2000US-0232080 2000US-0232081

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RESULT 3
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HTV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemie, atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder.
The present sequence is mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency
                                                                                                                                                                                                                                                                                                                    (NISB )
                                                                                                                                           Claim 1; Page 131-132; 174pp; Japanese
                                                                                                                                                                             allergies
                                                                                                                                                                                 Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies -
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DB; AAC55307.
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99JP-0178999.
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Pred. No.:
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colitis,
disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colitis, asthma, food allergy, drug allergy, allergic rhinitis, Roser disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevate IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the Fprotein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                          nervous system
                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; hamonomodulatory; concer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                        Claim 20;
                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                     WPI; 2001-514838/56
N-PSDB; AAI86953.
                                                                                                                                                                                               28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                07-SEP-2001
                                                                                                                                                                                                                                                                                          WO200164835-A2
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 20914.
                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO07022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO07022 standard;
                                                                                                                                                                     (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCCGACAT 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
asthma, food allergy, drug allergy, allergic rhinitis, Rosen
                        SEQ ID NO 20914; 1399pp + Sequence Listing; English
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2000US-0577409
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Matches:
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invention

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human polynucleotides

(AAI79941-AAI93841)

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AAB64608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                          Isolated nucleic acid molecule encoding a hunused in preventing, treating or ameliorating
                                                                                                                                                                                                  WPI; 2001-032312/04
                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
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                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US14934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                   a human secreted protein
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genes AAF32757-F32803 encoding

03-FEB-2000; 2000US-0496914 27-APR-2000; 2000US-0560875 05-FEB-2001; 2001WO-US03800

09-AUG-2001 WO200157188-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the human secreted proteins AAB64549-B64594. The sequence is used as a compary sequence for doing BLASTX searches to identify homologous sequences. The genes and proteins are useful for preventing, cameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune them therefore thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, reunatoid arthritis and ulcerative colitis; (c) cardiovascular colisorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; inmunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopath; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1568
1568
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein homologue, SEQ ID NO:1938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB11568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LeuGlnProProProProGlyPheLysArgPheSerCysLeuSerLeuProSerSerTrp
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                                                                                                                                                                                                                  osteopathic; vasotropic; cardiant;
vulnerary; antiulcer.
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RESULT 7
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                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC haematopoiesis regulatory activity; tissue growth activity;

CC haematopoiesis regulatory activity or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC inventon are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fingal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC may also be used in the diagnosis of the above conditions, and in drug

creening techniques. The present segments a novel human or
                                                                                                                                                                                                                      US-09-966-880A-7 (1-2818) x ABB11568 (1-88)
                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer - \,
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polypeptide of the in
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                                                                                                                                                          2054 CTGCAACCTCCAGCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGG
                                                                                                      1994 GATTACAGG 1986
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                                                              AspTyrArg 28
                                                                                                                                      {\tt LeuGlnProProProGlyPheLysArgPheSerCysLeuSerLeuProSerSerTrp}
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                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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2000US-0217487.
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08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232081. 2000US-0231968. 2000US-0232397. 2000US-0232398. 2000US-0232399.

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000;

2000US-0233065. 2000US-0234223.

2000US-0235484. 2000US-0235834. 2000US-0235836. 2000US-0236327.

2000US-0236367.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of novel human enzyme copyeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzhelmer's disease), metabolic disorders (e.g. phenylketonuria) inflammatory disorders (e.g. arthracia), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. hardiamatory disorders (e.g. infertility) and infectious disorders (e.g. infer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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  AA006720;
                                             AAO06720 standard; Protein; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                              1994 GATTACAGG 1986
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                                                                                                                                  AspTyrArg
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2000US-02510391.
2000US-0251030.
2000US-0251188.
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2000US-0251479.
2000US-02514868.
2000US-0251868.
2000US-0251869.
2000US-02519899.
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2000US-0249213 2000US-0249214 2000US-0249215 2000US-0249215 2000US-0249216 2000US-0249217 2000US-0249244 2000US-0249244 2000US-0249245 2000US-0249265 2000US-0249265 2000US-0249297 2000US-0249297 2000US-0249297 2000US-0249297

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0249212. 2000US-0246609. 2000US-0246610. 2000US-0246611. 2000US-0246613.

2000US-0246528. 2000US-0246532.

2000US-0249207. 2000US-0249208. 2000US-0246524. 2000US-0246525. 2000US-0246526. 2000US-0246527.

21-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 20-OC

2000US -0236368
2000US -0236369
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2000US -0237039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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             AAG01246 standard; Protein; 103
                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g.\ leukaemia, inflammation and immune
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                  inflammation.
                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                          2054 CTGCAACCTCCAGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGG
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                                                                                                 GATTACAGG 1986
                                                                  AspTyrArg 44
                                                                                                                          \texttt{LeuGlnProProProGlyPheLysArgPheSerCysLeuSerLeuProSerSerTrp}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs on DolyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and the full state of the sequences have been obtained, the full 5' ends and the full 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
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                                               AAU31902;
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                                                                                                                                                                                                                                                                           therapy;
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                                                                                          standard;
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                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                 The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agenists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
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                                   AAO02085 standard; Protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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26-JAN-2001; 2001US-0770160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                           2054 CTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the encoded proteins (AAOOOOIO-AAOI3910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 15977; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundiagnosing and treating e.g. leukaemia, inflammation and immundiagnosing and treating e.g. \frac{1}{2}
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18-MAY-2000; 2000US-0577409
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tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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                                                                                                         LeuGlnProProProProGlyPheLysArgPheSerCysLeuSerLeuProSerSerTrp 178
                                                                                                                                                              CIGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGG 1995
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                                                                                                                                                                                                                      CC polymerase chain reaction (PPR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC industrial dependence of the combinant production of (II). The CC industrial gene are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II), (II) is useful for generating antibodies against it, detecting or Quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II), (I) and (II) are useful for treating CC imaging of sites expressing (II), (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polypuclectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC diagnostics, forensics, gene mapping, identification of mutations CC diagnostics and produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC responsible for genetic this patent did not appear in the printed contribution of the polymeration of the polymerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic (
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                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 52437; 103pp; English.
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N-PSDB; AAS86265.
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23-AUG-2000;
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Gaps:
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Matches:
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Indels:
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US-09-966-880A-7 (1-2818) x ABG22078

(1-264)

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Best Local S. Query Match: DB:
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AAU31820
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                                                            Alignment Scores: Pred. No.: Score:
                                                                                                                                                       polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or CC physiological interactions of the polypeptide. Vectors comprising CC the nucleic acids encoding the polypeptides and cells genetically cengineered to express them are also useful for producing the proteins. They may be used to the proteins are useful in genetic vaccination, testing and concerning the polypeptides are growth or cartilage, tendon and/or nerve tissue growth or regeneration; cartilage, tendon and/or stimulation; as anti-inflammatory agents; and concerned former to leukaemias. AAUS3304 represent the amino acid commons of forces haven as anti-inflammatory agents.
                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
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                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                 of novel human secreted proteins of the invention
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                           Length:
Matches:
Conservative:
Mismatches:
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Query Match: DB:

Best Local Similarity: Percent Similarity:

5.6e-12 21.00 100.00% 100.00% 100.00% 2.34%

Conservative: Mismatches: Indels: Gaps: Matches:

000021

Score Alignment

No . .

Sequence

32

AA;

cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoisesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and

The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating

induce

Note: The sequence data for this patent did not specification, but was obtained in electronic for

format directly from WIPO

.nflammation.

at ftp.wipo.int/pub/published_pct_sequences

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RESULT 15
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18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                          Claim 20;
                                                                                                                                                                                     diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                     nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                    solated nucleic acids and polypeptides, useful for preventing iagnosing and treating e.g. leukaemia, inflammation and immun
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DB; AAI89253.
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-Q=Cgn2_1/USPTQ_spool/US09966880/runat_07072003_142234_22114/app_query.fasta_1.3015
-DB=Issued_patents_AA -OpWT=fastan -SUFFIX=olig.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRAUS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN-0 -MAXLEN-200000000
-USER-US09966880_@CGN_1_1_22=crunat_07072003_142234_22114 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-704-711A-1

US-09-521-220-1

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US-09-88-143-170

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6141.763 Million cell updates/sec
Sequence 121, App
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Sequence 121, App
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Sequence 171, App
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Sequence /, Ap Sequence 7, Ap	equence 7,	equence 7, A	equence 7, A	equence 53	equence 53	equence	equence 825	equence 4,	equence 4,	equence 4,	equence 4, Ap	equence 4, Ap	equence 4, Ap	equence 8	equence 43, A	equence 577,	equence 214,	equence 214,	equence 333,	equence 214,	equence 1, 🏞	equence 1	equence 4, F	equence 11,	equence 9, 🗜	equence 48,	equence 48,	equence 48,	equence 48,	equence 538,	eduction any

ALIGNMENTS

121, Application US/08454557C o. 5830670

TELEPHONE: (202) 371-2600 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 121 GENERAL INFORMATION: FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acid NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Neural Thread Protein of TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121 APPLICANT: de la Monte, APPLICANT: Wands, Jack | CITY: Washington STATE: D.C. COUNTRY: APPLICATION NUMBER: ADDRESSEE: 20005-3934 E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600 amino acids US/08/454,557C Suzanne 0609.3840003 Version Gene Expression and Detection

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                                                         US-09-966-880A-7 (1-2818) x US-08-340-426D-121 (1-375)
                                                                                                   Query Match:
                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                         Pred. No.:
                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                      US-08-340-426D-121
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino ~ ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neural Thread Protein Gene TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C
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1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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Sequence 22, Application US/09058489

Patent No. 6103886

GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489

CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
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Best Local Similarity:
Query Match:
DB:
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US-08-450-673C-121
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APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ludwid, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-MAY-199
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 20005-3934
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Best Local Similarity:
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US-09-058-489-22
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US-09-227-357-171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
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LENGTH: 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fischer et a TITLE OF INVENTION: 123 FILE REFERENCE; PZ010P1
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CURRENT FILING DATE: 1999-01-08
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                                                                                                                                                                                                                                                                         ER APPLICATION NUMBER: 60/051,918
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,920
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,733
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,795
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
                                                                                          ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,928
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-08-18
ER FILING DATE: 1997-08-18
ER FILING DATE: 1997-08-18
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                                           APPLICATION NUMBER: 60/055,948 FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/051,919
APPLICATION NUMBER: 60/055,949 FILING DATE: 1997-08-18
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Matches:
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Indels:
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Query Match:
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; LOCATION: (90)
; OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-7 (1-2818) x US-09-227-357-171 (1-90)
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TYPE: PRT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression :
TITLE OF INVENTION: Detection of Alzheimer's Disease
UNMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                    COUNTRY:
                                                                                                                                                                                            STREET:
                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,947
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,964
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/056,360
ER APPLICATION NUMBER: 60/055,684
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,984
ER FILING DATE: 1997-08-18
ER FILING DATE: 1997-08-18
ER FILING DATE: 1997-08-18
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,954
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/058,954
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/058,954
ER APPLICATION NUMBER: 60/058,954
ER APPLICATION NUMBER: 60/058,954
ER APPLICATION NUMBER: 60/058,785
ER FILING DATE: 1997-09-12
ER FILING DATE: 1997-09-12
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                                                                                                                    RY: U.S.A.
20005-3934
                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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Matches:
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APPLICATION NUMBER:

PCT/US95/17111A

PRIOR APPLICATION DATA:

CLASSIFICATION:

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                             APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20 NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-CCT-1994
PRIOR APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATLICIA D.
REGISTRATION NUMBER: 33,683
BEFERENCE TOCKET NUMBER: 33,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/340,426 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WILL, HOTST
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11 MOLECULE TYPE:
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 ELECOMMUNICATION INFORMATION:
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CITY: Washington
REFERENCE/DOCKET NUMBER: 33,683
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20007-5109
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                   26083/124
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RESULT 8
US-09-521-220-1
; Sequence 1, Application
; Patent No. 639348
; Patent INFORMATION:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL INFORMATION:
APPLICANT: WILL, HOTST
APPLICANT: WILL, HOTST
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTBASES, THEIR PRODUCTION AND
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: cUnknown>
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, Patricia D.
REGIGSTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
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                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09521220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20007-5109
                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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(202)672-5399
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17-MAR-1994
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Matches:
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LENGTH: 579 amino acids
TYPE: amino acid
STRANDEDNESS: single

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US-09-288-143-168
Sequence 168, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
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TITLE OF INVENTION: 53 Human Secreted Protein
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: FCT/US98/21142
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patentin Ver. 2.0
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SEQUENCE DESCRIPTION: SEQ
US-09-521-220-1
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens
US-09-288-143-170
                                                                                                                                                                                                                                                                                                                                                           US-09-966-880A-7 (1-2818) x US-09-288-143-170 (1-35)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 170
LENGTH: 35
                     APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     М
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Matches:
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Matches:
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EARLIER APPLICATION NUMBER: 60/061,463

EARLIER FILING DATE: 1997-10-09

EARLIER APPLICATION NUMBER: 60/061,529

EARLIER FILING DATE: 1997-10-09

EARLIER FILING DATE: 1997-10-09

EARLIER APPLICATION NUMBER: 60/061,527

EARLIER APPLICATION NUMBER: 60/061,527

EARLIER APPLICATION NUMBER: 60/061,527

EARLIER FILING DATE: 1997-10-09

EARLIER APPLICATION NUMBER: 60/061,536

EARLIER FILING DATE: 1997-10-09

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Best Local Similarity:
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EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,929
FILING DATE: 1997-07-08
                     FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,918
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,920
                                                                                                                       APPLICATION NUMBER: 60/051,916
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,930
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/052,803 FILING DATE: 1997-07-08 APPLICATION NUMBER: 60/052,732 FILING DATE: 1997-07-08
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APPLICATION NUMBER: PCT/US98/21142
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Indels:
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RESULT 12
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-227-357-285
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GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
                                                                                                                             Sequence 171, Application US/09288143 Patent No. 6433139
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LENGTH: 122
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EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
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EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1997-08-18
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EARLIER APPLICATION NUMBER: 60/058,660
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EARLIER APPLICATION NUMBER: 60/058,664
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APPLICATION NUMBER: 60/055,950
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,947
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-288-143-93
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-288-143-171
                                                                        Pred. No.:
                                                                                            Alignment Scores:
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EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
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Patent No. 6433139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER FILING DATE: 1998-10-08
                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
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EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
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EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER FILING DATE: 1997-10-09
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EARLIER FILING DATE: 1997-10-09
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FILE REFERENCE: PZ018P1
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                        LENGTH: 49
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Matches:
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:

Conservative: Mismatches:

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US-09-966-880A-7 (1-2818) x US-09-288-143-93 (1-49)
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APPLICANT: Fischer et
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EARLIER FILING DATE: 1998-07-07
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CURRENT FILING DATE: 1999-01-08
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ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,803
ER TILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,732
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,931
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,931
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,932
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ER APPLICATION NUMBER: 60/051,932
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
                     ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,964
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/056,360
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,684
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ER FILLING DATE: 1997-08-18
ER APPLICATION NÜMBER: 60/055,948
ER FILLING DATE: 1997-08-18
ER APPLICATION NÜMBER: 60/055,949
ER FILLING DATE: 1997-08-18
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BR APPLICATION NUMBER: 60/051,919

BR FILING DATE: 1997-07-08

BR APPLICATION NUMBER: 60/051,928

BR FILING DATE: 1997-07-08

BR FILING DATE: 1997-08-18

BR FILING DATE: 1997-08-18
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10. 634258
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APPLICATION NUMBER: 60/055,950
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,947
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,918
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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       1997-08-18
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Query Match:
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; TOPOLOGY:
US-08-454-557C-48
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                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, *
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557/
FILING DATE: 30-MAX-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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EARLIER APPLICATION NUMBER: 60/C
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
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                                                                                       TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, Suite 600
                                                                  LENGTH:
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ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/058,785
ER FILING DATE: 1997-09-12
ER APPLICATION NUMBER: 60/058,664
ER FILING DATE: 1997-09-12
ER APPLICATION NUMBER: 60/058,660
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                                          amino acid
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           Score
 198
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                                                  Query
Match Length
                                                                                                                                                                  Xgapop 60.0
Ygapop 60.0
Fgapop 6.0
Delop 6.0
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897
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4.7
2.1
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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US-09-966-880A-2
US-10-106-698-5145
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60.0
7.0
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Sequence 8, Appli
Sequence 2, Appli
Sequence 5145, Ap
Sequence 803, App
                                                   Description
 Alignment Scores
                        US-09-966-880A-8
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                                                          SOFTWARE: FastSEQ
SEQ ID NO 8
LENGTH: 198
                                                                                                                                                                                                                                                                                    Sequence 8, Application US Patent No. US20020164743A1
                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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ALIGNMENTS

US-10-011-585A-154
US-09-764-891-356
US-09-764-891-4746
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US-09-925-299-1013
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US-10-198-070-30

Sequence 154, App Sequence 3556, Ap Sequence 4746, App Sequence 45, Appl Sequence 41013, Ap Sequence 1013, Ap Sequence 1013, Ap Sequence 214, Appl Sequence 214, Appl Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1056, Ap Sequence 1056, Ap Sequence 1151, Ap Sequence 171, Appli Sequence 172, Appli Sequence 1735, Appli Sequence 1735, Appli Sequence 174, Appli Sequence 175, Appli Sequence 177, Appli Sequen

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APPLICANT: Honjo, Tasuku
APPLICANT: MUZAMATSU, MASAMICHI
APPLICANT: MUZAMATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09966880A Patent No. US20020164743A1
                                                                                                                                                                                                                                                                   APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGluProGluGlyLeuArgArgLeuHlsArgAlaGlyValGlnIleAlaIleMetThr
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PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN Ver. 3.0
IN NO 5145
LENGTH: 59
TYPE: PRI
DECEMBER OF TABLES                                                                                                                                                                                       US-09-925-302-803; Sequence 803; Application in Patent No. US20020044941A1; GENERAL INFORMATION:
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Query Match:
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Query Match:
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                  US-09-764-891-3556
Sequence 3556, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Query Match:
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US-10-011-585A-154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0261
CURRENT APPLICATION NUMBER: US/10/011,585A
CURRENT APPLICATION NUMBER: US/10/011,585A
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/245,740
PRIOR APPLICATION NUMBER: 60/245,740
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 245
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 803
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                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
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TYPE: PRT
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TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TITLE OF INVENTION: CONDITIONS REQUIRING THE TITLE OF INVENTION: CELLS
FILE REFERENCE: 59003.00008
CURRENT APPLICATION NUMBER: US/10/198,070
CURRENT FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,161
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/306,150
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
TRIOR APPLICATION NUMBER: 60/331,477
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 79
LENGTH: 368
TYPE: PRIOR SERVICE S
US-09-966-880A-7 (1-2818) x US-10-198-070-79 (1-368)
                                                                                              Query Match:
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                                                                                                                              Best Local Similarity:
                                                                                                                                                          Percent Similarity:
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Publication No. US20030109437A1
GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
APPLICANT: GEMMELL, JACK
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NUMBER OF SEQ ID NOS: 10331
SOFTWARE: PatentID Ver. 2.0
SEQ ID NO 3556
LENGTH: 147
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                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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RESULT 9
US-10-001-873-34
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US-09-764-891-4746
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
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SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4746
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                                                                                                                                                                                                                                               APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0275
CURRENT APPLICATION NUMBER: US/10/001,873
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,055
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,496
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: DET/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SEQ ID NO 1013

LENGTH: 25

TYPE: PRT

ORGANISM: Homo sapiens
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                 Alignment Scores: Pred. No.:
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US-09-925-299-1013
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PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/306,150
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/331,477
PRIOR FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 125
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SEQ ID NO 45
LENGTH: 133
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FILE OF INVENTION: CELLS
FILE REFERENCE: 59003.000008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/198,070 CURRENT FILING DATE: 2002-07-19
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1013
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US-09-925-299-1013
, Sequence 1013, Application US/09925299
, Patent No. US20020055627A1
                                                                                                                                                                                      APPLICATION UMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 00/124,270
PRIOR FILING DATE: 1999-03-12
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
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TYPE: PRT
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ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,884
ER FILING DATE: 1997-06-06
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               APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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                                                                               APPLICATION NUMBER: 60/048,972 FILING DATE: 1997-06-06
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LOCATION: (79)
OTHER INFORMATION:
US-10-023-282-781
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
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EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
Sequence 24, Application US/10198070
Publication No. US20030109437A1
GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
APPLICANT: GEMMELL, JACK
TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUNORS AND TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION
TITLE OF INVENTION: COLLS
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SOFTWARE: PatentIn Ver. 2.4
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/048,883
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APPLICATION NUMBER: 60/048,897
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FILE REFERENCE: 59003.000008

CURRENT APPLICATION NUMBER: US/10/198,070

CURRENT FILING DATE: 2002-07-19

PRIOR APPLICATION NUMBER: 60/306,161

PRIOR FILING DATE: 2001-07-19

PRIOR PILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR PILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 125

SOFTWARE: PATENTIN VET. 2.1

SEQ ID NO 24
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Query Match:
Search completed: July Job time: 72 secs
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-Q-/cgn2_1/USPTO_spool/US09966880/runat_07072003_142233_22095/app_query.fasta_1.3015
-DB=PIR_73 -QFMT=fastan -SUFFIX=0lig.rpr -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40_cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN=-20000000000
-USER=US09966880_GCGN_1_1_72_grunat_07072003_142233_22095 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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ALIGNMENTS

A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-627 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived |
A; Reference number: A40200; MUID: 92241891; PMID: 1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6
in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequenc RESULT C40201 artifact-warning sequence (translated ALU class A) - human C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 C;Accession: A40201 R;Claverie, J.M. В δÃ Percent Similarity:
Best Local Similarity:
Query Match: A; Accession: A40201 personal communication, 1992 A; Reference number: A40201 A40201 US-09-966-880A-7 (1-2818) x A40201 (1-627) Alignment Scores: .. N 3.02e-06 15.00 100.00% 100.00% 1.67% Conservative: Mismatches: Indels: Gaps: Length: Matches: protein sequence 0 0 0 0 all 6 reading frames and other potenti to a portion of

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RESULT 4
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artifact-warning :
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Query Match:
DB:
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A;Rocession: S01441
A;Molecule type: mRNA
A;Residues: 1-296 <CAI>
A;Cross-references: EMBL:X12544; NID:g32210; PIDN:CAA31061:1; PID:g32211
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1988
A;Note: only part of the sequence is given
A;Note: the authors translated the codon TTT for residue 266 as Gly
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-296/Product: class II histocompatibility antigen, HLA-DR beta-1 chain #status
F;139-204/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              class II histocompatibility antigen HLA-DR beta-1 chain precursor (clone LS1.1.1) (C.Species: Homo sapiens (man) (C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000 (C.Accession: S01441 R.Curtsinger, J.M.; Bach, F.H. Nucleic Acids Res 16, 9353, 1988 A;Title: Identification of a novel DR beta cDNA clone. A.Reference number: S01441; MUID:89016649; PMID:3174462
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C;Comment: Any significant similarity of a predicted protein
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A:Title: Identifying coding exons by similarity search: Alu-derived and other
A:Reference number: A40200; MUID:92241891; PMID:1572661
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A;Reference number: A40201
A;Accession: C40201
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R;Claverie, J,
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artifact-warning sequence (translated
C; Species: Homo sapiens (man)
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RESULT 5
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C;Comment: Any significant similarity of a predicted protein sequen
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A;Title: Identifying coding exons by similarity search: Alu-derived
A;Reference number: A40200; MUID:92241891; PMID:1572661
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C;Comment: Any significant similarity of a predicted protein sequence to a portion of the content o
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A; Residues: 1-597 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search:
A; Reference number: A40200; MUID:92241891; PMID:1572661
RESULT
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R;Claverie, J.M
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C:Date: 31-Mar-1992 #sequence
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personal communication, 1992
A:Reference number: A40201
A:Accession: F40201
A:Molecule type: DNA
A:Residues: 1-673 <CLA>
R:Claverie, J.M.
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Genomics 12, 838-841, 1992

A;Title: Identifying coding exons by similarity search: Alu-derived and (A;Title: Identifying coding exons by similarity search: Alu-derived and (A;Reference number: A40200; MUID:92241891; PMID:1572661

A;Reference number: A40200; MUID:92241891; PMID:1572661

A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 rea in-frame stop codons are shown as 'X'.
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C;Accession: F403
R;Claverie, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine/threonine-specific protein kinase (EC 2.7.1.-) STK2 - human (Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999 (C)Accession: 178885 (R)Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, Oncogene 9, 1977-1988, 1994 (R)Ttle: Two novel human serine/threonine kinases with homologies to the cell A;Reference number: 158396; MUID:94268838, PMID:8208544 (R)Accession: 178885
                                                                                                                                                                                                                                                                                                                                               C; Keywords: phos
F; 4-261/Domain:
MHC HLA-DR-beta-1 chain - C; Species: Homo sapiens (m
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A;Map position: 3p21.1-3p21.1
C;Superfamily: human serine/threonine-specific
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Best Local Similarity:
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A;Residues: 1-841 <RES>
A;Cross-references: GB:L20321; NID:g348244;
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                                                                                    1839 TGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 18:
                                                                                                                                                                                                                                                                                                                                                                   phosphotransferase
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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A; Accession type; mRNA
A; Molecule type; mRNA
A; Residues: 1-114 <SOS>
A; Note: the authors translated the codon G
A; Note: the authors translated the codon G
A; Molecule type: DNA
A; Residues: 1-301 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
                                                                         A; Reference number: A40201
A; Accession: B40201
                                                                                                                                              artifact-warning sequence (translated C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision C;Accession: B40201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Sosa, M.A.G.; De Gasperi, R.; Battistini, S.; Gorman, M. Biochem. Biophys. Res. Commun. 227, 636-641, 1996
A;Title: A human kidney cDNA which induces a cell surface A;Reference number: JC5238; MUID:97032815; PMID:8878564
A;Contents: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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A; Residues: 1-47 <RES>
A; Cross-references: GB:M15073; NID:g188370; PIDN:AAA59814.1; PID:g3
A; Cross-references: GB:M15073; NID:g188370; PIDN:AAA59814.1; PID:g3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 31-May-1996 *sequence_revision 31-May-1996 *text_change 23-Jul-1999 C;Accession: 179424
R;Gregersen, P.K.; Shen, M.; Song, Q.
Proc. Natl. Acad. Sci. U.S.A. 83, 2642-2645, 1986
A;Title: Molecular diversity of HLA-DR4 haplotypes.
A;Reference number: I59062; MUID:86206008; PMID:3458223
A;Accession: I79424
                                                                                                                               R; Claverie, J.M.
                                                                                                                                                                                                                                                                           B
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Best Local Similarity:
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 07-May-1999
                                                                                                            personal communication,
                                                                                                                                                                                                                       B40201
                                                                                                                                                                                                                                        RESULT 10
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ongs to
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Identifying coding

exons by

similarity

search:

Alu-derived

and

other

potenti

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-597 <CLA>
R; Claverie, J.M.
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potential
A; Title: Identifying coding exons by similarity search: Alu-derived and other potential
A; Reference number: Ad0200; MUID:92241891; PMID:1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames of
in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of t
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E40201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Catesion: E40201
D;Catesion: E40201
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A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation
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A;Molecule type: mRNA
A;Residus: 1-391 <KOE>
A;Cross:references: EMBL;AL117444
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C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A40201
A; Accession: E40201
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Best Local Similarity:
Query Match:
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A; Accession: T17239
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Gaps:
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Conservative:
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                                                    Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading f in-frame stop codons are shown as 'x'.
C;Comment: Any significant similarity of a predicted protein sequence to a por
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-673 <CLA>
R; Claverie, J.M.
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A; Accession: F40201
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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-627 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potenti
A; Title: Identifying coding exons by similarity search: Alu-derived and other potenti
A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames o
in-frame stop codons are shown as 'x'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of
               C; Accession: F40201 R; Claverie, J.M.
                                                     C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995
                                                                                          artifact-warning
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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A;Reference number: A40201
A;Accession: A40201
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C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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A;Experimental source: cultivar Columbia
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I; Town, C.D.; Fujii, C.Y.;
M.; KOO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84623
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A;Residues: 1-773 <STO>
A;Cross-references: GB:AE002093; NID:g2642433; PIDN:AAB87101.1; GSPDB:GN00139
Search completed: July 7, 2003, 23:38:59 Job time: 69.5 secs
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A; Map position: 2
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A;Molecule type: DNA
A;Residues: 1-773 <ROUD
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Database: SwissProt_40:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result Query No. Score Match Length DB ID C 1 23 2.6 585 1 ALU5_HUMAN C 2 23 2.6 591 1 ALU8_HUMAN C 2 23 2.6 593 1 ALU7_HUMAN C 3 2.3 2.6 593 1 ALU7_HUMAN C 4 22 2.3 2.6 593 1 ALU7_HUMAN C 5 21 2.3 585 1 ALU5_HUMAN C 6 21 2.3 591 1 ALU8_HUMAN C 7 2 2.3 591 1 ALU8_HUMAN C 8 20 2.2 587 1 ALU8_HUMAN C 9 20 2.2 587 1 ALU8_HUMAN C 9 20 2.2 587 1 ALU8_HUMAN C 11 18 2.0 593 1 ALU4_HUMAN C 11 18	DB DC B D	Copy. - protein so July Tuly ore: 897 1 agagop
RR SEQUENCE FROM N.A. RR SEQUENCE FROM N.A. RR SEQUENCE FROM N.A. RX MEDILINE-95021758; PubMed-7935834; RA Claverie JM., Makalowski W.; RT 141 alert."; R1 Nature 371:752-752(1994). RP CONCEPT. RN [2] RP CONCEPT. RX MEDILINE-92241891; PubMed-1572661; RA Claverie JM.; RA J. M. M. J. M.	ALIGNMENTS RESULT 1 ALU5_HUMAN STANDARD; PRT; 585 AA. ID ALU5_HUMAN STANDARD; PRT; 585 AA. AC p39192; DT 01-FEB-1995 (Rel. 31, Created) DT 01-FEB-1995 (Rel. 31, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DT 14-OCT-2001 (Rel. 40, Last annotation warning entry. DE Alu subfamily SC sequence contamination warning entry. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX MCBI TRATD-8606:	C 19 11 1.2 629 1 2195_HUMAN

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- MISCELLANEOUS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIEDD BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSCRIEDTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CONA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBLITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONCENTRANCE AND THE POSSIBLITY THAT THE MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE POSSIBLITY THAT THE MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SECUENCING THE POSSIBLITY THAT THE MAY HAVE AND THE POSSIBLITY THAT THE PROPERTY HAVE NOT THE POSSIBLITY THAT THE MAY HAVE AND THE POSSIBLITY THAT THE
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"Identifying coding exons potentially misleading pro-
Genomics 12:838-841(1992).
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MEDLINE=91178815; PubMed=1706781;
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J. MOI. EVOI. 32:105-121(1991).

J. MOI. EVOI. 32:105-121(1991).

THAT ALU REPEATS FALL INTO 8 SUBBAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTEANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTEANSCRIPTED REGIONS. HOWEVER, CONA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTARION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE PRESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM A CONTAIN OF THE NEADING FRAME MAY HAVE RESULTED FROM AND TH
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                                                                                                                                                                                                                                                                CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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CODING NUCLEOTIDE SEQUENCE.
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                                                  ION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL: U14574; -; NOT_ANNOTATED_CDS.
Hypothetical protein.
Hypothetical protein.
1 96 FRAME-1.
DOMAIN 109 294 FRAME-3.
DOMAIN 109 393 FRAME-4.
DOMAIN 397 492 FRAME-5.
DOMAIN 397 492 FRAME-5.

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A RESOLUTION OF A CONCRETE REPORT OF A CONCRETE REP
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01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                           Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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P39194;
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Mammalia; Eutheria; Primates;
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARTES ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
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CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS
CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER
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OVIDED IN ORDER TO AVOID THE FURTHER
DATABASES WITH ALU-DERIVED AMINO
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 Claverie J.-M.;
"Identifying coding exons by similarity search:
potentially misleading protein sequences.";
Genomics 12:838-841(1992).
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Claverie J.-M., Ma
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NCBI_TaxID=9606;
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Mammalia; Eutheria;
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GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOXED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SP sequence contamination warning 371:752-752(1994) STANDARD; Makalowski W.; PubMed=1572661; PubMed=7935834; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. Ã entry. alu-derived

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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
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Mammalia; Eutheria;
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Alu alert.";
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                                                 CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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Jurka J., Milosavljevic A.; "Reconstruction and analysis of J. Mol. Evol. 32:105-121(1991).
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Mammalia; Eutheria;
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15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
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                                                                    u family developed through successive waves of fixation connected with primate lineage history."; Evol. 27:194-202(1988).
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          analysis of human Alu
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FRAME-3.
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CONA LIBERARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS.
LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME O
ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPETS MAY
ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS.
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AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
NG NUCLEOTIDE SEQUENCE.
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Query Match: Score: Alignment Scores: Pred. No.: DOMAIN DOMAIN SEQUENCE This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). DOMAIN DOMAIN DOMAIN Hypothetical DOMAIN EMBL; U14574; -; NOT_ANNOTATED_CDS 100 199 298 397 496 591 protein ÃĄ. 1.53e-12 21.00 100.00% 100.00% 2.34% 195 195 294 393 492 591 64395 MW. FRAME-1. FRAME-2. FRAME-3. FRAME-4. FRAME-6.
AC8154AD8A6BB280 CRC64; FRAME-5. Length: Matches: Conservative: Gaps: Mismatches: Indels: 000022

US-09-966-880A-7 (1-2818) x ALU8_HUMAN (1-591)

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RESULT P39194; 01-FEB-1995 01-FEB-1995 16-OCT-2001 Alu subfamil ALU7_HUMAN -FEB-1995 (Rel. 3 -FEB-1995 (Rel. 3 -OCT-2001 (Rel. 4 u subfamily SQ se 2053 1993 TCCCAGCTACTTGGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGGTGGAGGTTGC 154 174 AGT SerGlnLeuLeuGlyArgLeuArgGlnGluAsnArgLeuAsnProGlyGlyGlyGlyCys STANDARD; 31, 31, 40, Last sequence update)
Last annotation updat Created) t annotation update) contamination warning PRT; 593 2052

entry

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closely J. Mol.
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DOMAIN
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CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISSINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
                                                                                Hypothetical protein DOMAIN 1
                                                                                                                                                                                 use by non-profit institutions as lon modified and this statement is not removentilies requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=95021758; PubMed=79
Claverie J.-M., Makalowski
"Alu alert.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                            between
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J. Mol. Evol. 32:105-121(1991).

-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91178815; PubMed=1706781;
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CAUTION: ANY SIGNIFICANT SIMILARITY OF A DUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
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LINE=88333009; PubMed=3138422;
                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ACID SEQUENCES.
CAUTION: ALU REPETITIVE SEQUENCES ARE INTERS:
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-i- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDIC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1995 (Rel. 31, Last sequence up
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P39189;
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ACID SEQUENCES.
CAUTION: ALU REPETITIVE
PRIMATE GENOMES WITH AN
ACTIVELY TRANSCRIBED BY
                                                                                  MISCELLANBOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASE CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTH POLLUTION OF PROTEIN SEQUENCE DATABBASES WITH ALU-DERIVED AMINO POLLUTION OF PROTEIN SEQUENCE DATABBASES WITH ALU-DERIVED AMINO PROTEIN SEQUENCE DATABBASE PROTEIN SEQUENCE PROTEIN SEQ
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  SEQUENCES ARE INTERSPERSED IN HUMAN AND AVERAGE SPACING OF 4 KB. SOME OF THEM AI POL III. NORMAL TRANSCRIPTS MAY CONTAIN
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Query Match:
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16-OCT-2001 (Rel. 40, Last
Alu subfamily SB1 sequence
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P39190;
"Identifying coding exons by similarity search: potentially misleading protein sequences."; Genomics 12:838-841(1992).
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                                                                                                                            Claverie J.
                                                                                                                                                        MEDLINE-92241891;
                                                                                                                                                                                                                                                                                Nature 371:752-752(1994)
                                                                                                                                                                                                                                                                                                                                                    Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95021758;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REBARRANCED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMBNYS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
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J. MOI. Evol. 32:105-121(1991).

-I-MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEAS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARR
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRANCES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urka J., Milosavljevic A.;
                                                                                                                                                                                                                                      BEING REPORTED.

CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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                                                                                                                                                                                                                              CODING NUCLEOTIDE SEQUENCE.
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Percent Similarity: Best Local Similarity: Query Alignment Scores: DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Hypothetical DOMAIN EMBL; ĕ :. Match: U14569; 100 198 296 395 493 protein -; NOT_ANNOTATED_CDS 1.61e-11 20.00 100.00% 100.00% 2.23% 96 194 292 391 489 587 63573 ¥. FRAME-3. FRAME-4. FRAME-6 FRAME-5 FRAME-1. 85C4155726DEF235 Matches: Conservative: Mismatches: Indels: 587 0 0 0

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http://www.isb-sib.ch/announce/

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                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO ACID SEQUENCES.
-!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARLES ALSO CONTAIN APRILAL AND/OR REARRANGED CDNAS.

LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONNIC ARTHEACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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01-FEB-1995 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "RECONSTRUCTION and analysis of human Alu genes.";

J. MOI. Evol. 32:105-121(1991).

-I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING

CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX

FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Jurka J., Milosavljevic A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identifying coding exons by similarity search: alu-derived and potentially misleading protein sequences."; Genomics 12:838-841(1992).
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Alu subfamily SP sequence contamination warni
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3009; PubMed=3138422;
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Jurka J., Milosavljevic A.;
                                                                                                                                               "The Alu family developed through successive waves closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
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Eukaryota; Metazoa; Chordata; Craniata; Vertehr Mammalia, Puthanan
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                                                                                 "Reconstruction and analysis of J. Mol. Evol. 32:105-121(1991).
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB2 sequence contamination warning entry.
Homo sapiens (Human)
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                                                                           Claverie J.-M., Makalowski W.;
"Alu alert.";
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J. MOL. Evol. 32:105-121(1991).

THAT ALU REPEATS FALL INTO 8 SUBPAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORWAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATIVE ALU-DERIVED SEQUENCE IN ANY ORIENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALIERWATIVE EXONS, CONSLIDERATION SHOULD BE GIVEN TO THE POSSIBLITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARRIFACT OR MAY BE DUE TO MISTIARRATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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Claverie J.-M., Makalowski
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J. Mol. Evol. 32:105-121(1991).
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                             BEING REPORTED.
CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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J. Mol.
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
                                                                                                          MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
                                                                                                                                                                                                                                                                                                                                                                 "Identifying coding exons by similarity search: potentially misleading protein sequences."; Genomics 12:838-841(1992).
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                                                                                                                                    ALU FAMILIES CLASSIFICATION
MEDLINE-91178815; PubMed-17
                                                                                                                                                                                                                                                                          Quentin Y.;
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RESULT 15
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                                                                                                                   ALU1_HUMAN STANDARD; PRT; DYL MA. P39188; C1-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Alu subfamily J. Sequence contamination warning entry.
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SEQUENCE FROM N.A. MEDLINE-95021758;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Search completed: July 7, 2003, 23:33:14 Job time: 46.5 secs

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Command line parameters:

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-DB-SPTREMBL_21 -OPMT=fastan -SUFFIX=olig.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START-1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENN=0 -MAXLENN=2000000000
-USER=US09966880_@CGN_1_1_155_@runat_07072003_142233_22077 -NCPU=6 -TCPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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ALIGNMENTS

Euteleostomi; Murinae; Mus

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Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/uubu ....
EMBL; AB040431; BAB12721.1; -.
EMBL; AB040430; BAB12720.1; -.
EMBL; BC006296; ABH06296.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo
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TISSUE-TESTIS,

SITUSBERG R.;

SUBMITTED (MAR-2002) to the EMBL;

BC024651; AAH24651.1; -.

SEQUENCE 72 AA; 8162 MW; (
                                                                                                                                                                                                                                                          Q8TB48; PRELIMINARY;
Q8TB48;
01-JUN-2002 (TrEMBLRE1. 2
01-JUN-2002 (TrEMBLRE1. 2
01-JUN-2002 (TrEMBLRE1. 2
                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                 Similar to PRO2550
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MGD; MGI:1342279; Aicda.

InterPro; IPR002125; dCMP/Cyt_deam.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davidson N.O., Honjo T.; "Specific expression of activation-induced cytidine novel member of the RNA-editing deaminase family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
Transformation related protein (Fragment).
                                                                                                                                                                                                                                                                            Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.,
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDJ databases.
EMBL; AKO23582; BAB14616.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09H8KO;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ13520 fis, clone PLACE1005828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L24
NON_TER
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shen H., Steinberg M.L.;
Submitted (SEP-193) to the EMBL/GenBank/DDBJ
EMBL; L24521; AAA36776.1; -.
NON_TER 1 1
TOTAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q15662
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TISSUE=PLACENTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2039 CCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGG
                                                                                                                                                                                                                        Scores:
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                                                                   2.52e-08
17.00
100.00%
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1.89%
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Wakamatsu
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   ADD DE RAP DE RA
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Q9NWF0
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Best Local Similarity:
Query Match:
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Q96QL7
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                                                                                                                                 C TISUE=EMBRYO;

I ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

I Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Bara H.,

I Mishikawa T., Nagai K., Sugano S., Takahashi-rujii A., Hara H.,

I A Arita M., Nabekura Y., Toqiya S., Komai F., Hara R., Takeuchi K.,

IA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

IA Arita M., Nabekura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project."

"NEDO human cDNA sequenc
PROSITE; PS00036; BZIP_BASIC;
DNA-binding; Nuclear protein.
SEQUENCE 423 AA; 46463 MW;
                                                                                      PRINTS; PRO0041; LEUZIPPRCREB SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Eypothetical 46.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008394; AAH08394.1; -. SEQUENCE 318 AA; 33894 MW; D70E20D5409C165B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Similar to cAMP responsive element binding protei
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Q96QL7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Primates;
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348A5EFEC5A1E977
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Matches:
Conservative:
Mismatches:
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Suzuki Y.,
Hara H.,
ikeuchi K.,
zamamoto J.,

Alignment Pred. No.:

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Alignment Scores:
Pred. No.:
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Best Local Similarity:
Query Match:
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01-OCT-2000 (
01-OCT-2000 (
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ISOGAL T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Magatsuma M., Othiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK02493; BAB14823.1; -.
EMBL; AK02493; BAB14823.1; -.
EMBL/Seprencing Project."
Watanabe K., Kumagai
Suzuki Y., Obayashi N
Nakamura Y., Isogai 1
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence up
01-0CT-2000 (TrEMBLrel. 15, Last annotation
CDNA FLJ20495 fis, clone KAT08572.
                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                   Q9NX13
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Isogai T., Ota
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TYEMBLYE1. 16, Created)
01-MAR-2001 (TYEMBLYE1. 16, Last sequence update)
01-COT-2001 (TYEMBLYE1. 18, Last annotation update)
Hypothetical 17.1 kDa protein.
                                                                          SEQUENCE
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                                                                          FROM
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                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                       Chordata;
Primates;
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i A., Itakura S.,
M., Nishi T., Sh
T., Sugano S.;
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                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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Catarrhini; Hominidae;
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Matches:
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ibahara T.,
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SEQUENCE FROM N.A.

Barlund M., Monni O., Weaver D.J., Kallioniemi A.;

Barlund M., Monni O., Weaver D.J., Kallioniemi A.;

"Cloning of two novel genes, BCAS3 and BCAS4, that are a

"Cloning of two novel genes, BCAS3 and BCAS4, that are a

"Cloning of two novel genes, BCAS3 and BCAS4, that are a

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01-OCT-2000
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                SEQUENCE FROM N.A.
MEDILNE=20319030; PubMed=10861003;
Shen P., Wang F., Underhill P.A.,
Sung R., Lin A.A., Hyman R.W., Vol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "NEDO human CDNA sequencing pasubmitted (FEB-2000) to the ENEMEL; AKO00502; BAA91209.1; -SEQUENCE 181 AA; 19669 MW;
                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Ubiquitous TPR-motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Homo sapiens (Human).
Chordata;
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01-JUN-2002 (TrEMBLrel 21, Last sequence up
01-JUN-2002 (TrEMBLrel 21, Last annotation
Breast carcinoma amplified sequence 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NR08
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                                                                                                                                                                                                                                                                                                                                   (TIEMBLrel. 15, Created)
(TIEMBLrel. 15, Last sequence update)
(TIEMBLrel. 15, Last annotation updat
TPR-motif protein Y isoform (Fragment)
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Primates;
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R.W., Vollrath
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EMBL/GenBank/DDBJ
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Catarrhini;
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(Fragment).
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Davis
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CDNA: FLJ23147 fis, clone LNG09295.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Primates; Catarrhini; Hominid
                                                                                                   060448 PRELIMINARY; PRT; 375 AA. 060448; 01-AUG-1998 (TREMBLrel. 07, Created) 01-AUG-1998 (TREMBLrel. 07, Last sequence update) 01-DEC-2001 (TREMBLrel. 19, Last annotation update) Neuronal thread protein AD7c-NTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AKO26800; BAB15557.1;
SEQUENCE 232 AA; 26703 MW; 56946BE74C226FU
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Proc. Natl. Acad. Sci. U.S.A.
EMBL; AF265575; AAF77052.1; -.
NON_TER 1 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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genetic implications
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Catarrhini;
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i; Hominidae; Homo.
                                                        Vertebrata; Euteleostomi;
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Homo sapiens (Human).
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SEQUENCE FROM N. F
TISSUE=NEURONAL;
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                                                                                    Q96LU6 PRELIMINARY; PRT; 166 AA. Q96LU6; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence up 01-DEC-2001 (TrEMBLrel. 19, Last annotation CDNA FLJ25058 fis, clone CBL04608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional prediction of the coding sequences of 33 new by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFI18081; AAF22025.1; -
SEQUENCE 126 AA; 13439 MW; 183EFE16B1D25C91 CRC64;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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Primates;
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Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2003 Compus
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No.	Score	Query Match Length DB ID	Length	B	ID	Description
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2	2174	77.1	6564	21	AAC55314	Human activation-i
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4	2172	77.1	2172	21	AAC55319	
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6	574	20.4	574	22	AAK81089	-
7	429	15.2	429	22	AAK61819	_
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ALIGNMENTS

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NO:7

Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; altergy; altergic disease; antiallergic; antianemnic; antiasthmatic; ophthalmological; anti-HIV; dermatological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food altergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; altergic colitis; Rosen disease; DiGeorge disease; AIDS; drug altergy; altergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disease; major histocompartibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.

sapiens.

05-OCT-2000 WO200058480-A1. 80..676 /*tag= a
/product= "activation-induced Location/Qualifiers cytidine deaminase"

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Best Local Sin
Matches 2818;
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24-JUN-1999;
27-DEC-1999;
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a target for drug development for
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allergies Nucleic acid a target for acid encoding activation induced cytidine for drug development for immune-related d diseases deaminase, useful including as

Claim 17; Page 145-150; 174pp; Japanese

The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences

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AGGAAAATCT:	ACAAACTTCAC	\GTAGCAAATC \GTAGCAAATC	atcttaaat atcttaaaat	TATGGGTGGG	DATGCGCTGTA DATGCGCTGTA	VATGAGAGTATI VATGAGAGTATI	IGACGTTTACT GACGTTTACT	TATTTGATTC	BAAGGTAGATO BAAGGTAGATO	BACCTGGGAGC	CTGCAATTGGT CTGCAATTGGT	PCTTTAAAAAG CTTTAAAAAG	IGTTTTTATTC	CACACGATGAA CACACGATGAA	SATGACTTACG SATGACTTACG	%; Score 2174; 0%; Pred. No. 0; 0; Mismatches	358
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TGGGTCTCTTC	AGCAAACAATT	CAAACTCTTT CAAACTCTTT	CTGTGAACAAG CTGTGAACAAG	AGACCATGCAT	GCAGAAGCATG - - - - - - GCAGAAGCATG	TGACCCCAAAC TGACCCCAAAC	CAAACTCTTCC CAAACTCTTCC	CAGTGGTGTT# CAGTGGTGTT#	GGTGAGAGGAI GGTGAGAGGAI	TCAACGTTTT	TGCAACATTG1	GAAAATAGAG <i>I</i> GAAAATAGAG <i>I</i>	CTTTCTTAGAC	GAAGACAGTGO	GTACTTTGGG!	1; Length 6 0; Indels	ssis and treatment of these disorders genomic DNA sequence of human AID. C; 1383 G; 1914 T; 0 other;
CTTGAATGTTGGGGAGAGGAAAATCTATTGGCTCTCGTGGGTCTCTTCATCTCAGAAAT	**AATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAAACAATTGGAAGGAA	ATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCC 	AGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCCTAATA	GTACAAAAGAAGATTGTTATGGGTGGGGATGGAGGTATAGACCATGCATG	AGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAGAAGCATGTTTTTATGTTT	ATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTCTCCAA	TICTATICTITICCOTIGACGITTACTITCAAGTAACACAAACTCTITCCATCAGGCCATG	GTGATAGATTT GTGATAGATTT	AGGTAGGATGAGAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGAGGATCAAATGTTTTT	CTATGACTTTT	CCCCTACTGG	AATATTTATATACGACTCTTTAAAAGATCTATGTCTTGAAAATAGAGAAGGAACACAGG 	TTTACAGAAAA TTTACAGAAAA	ACTTCCAGGAATGTCACACACGATGAAATATCTCTGCTGAAGACAGTGGATAAAAAAACAG	ACTTTGATAGO: ACTTTGATAGO:	0; Gaps	•
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TTTAGTAAACTTTTATGACAGCAAA;		GATTITTATTAACATGATTCCTTTTCTGATATATAAAAGCTTCAAAGCTTCAAAGCTTCATTCCTTTTCTGATATGAAATGAAATCTTCAAGCTTCAT	AAGAGTTAAAAATTGTTACTTCATGTAFTCATGTATTTATATTTATATTATTTTGCGTCTAAT	CACAGGAAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTTTGTAA	AATAACCATATCCCTGTGCCGTTATTACCTAGCAACCCTTGCAATGAAGATGAGCAGATC	GTCTCTTTTGGTGTCTATTTGTCCCTAACAACTGTCTTTGACAGTGAGAAAATATTCAG 	TTGCAAGGAAATTGTGCTTTATCCAACAAATGTAAGGAGCCAATAAGGGATCCCTATTT	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGATICTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCAGAAAAAAA	CTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTG	TCTGTACTCAAAATGCAAAATTAGCCAGCGTGGTAGCAGGACCTGTAATCCCAGCTA 	CGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAACCCCG	AGAGAGAGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGC	AGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCAAAAAAAA	CTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGGATGGCTTGAACACAGGTGTTCA	TTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACG 	GCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGTG

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treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency diseases IGA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic trinitis, Rosen disease, Diceorge disease, ataxia telangicetrasia, common variable immunodeficiency disease, MRC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
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a target Nucleic acid for drug encoding development activation induced cytidine deaminase, useful as elopment for immune-related diseases including including

WPI;

2000-611715/58

Claim 18; Page 152-153; 174pp; Japanese

The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disease, ataxia telangiectasia, common variable ilmunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences

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                                                                                                                                                                                                                                    amino acid sequences given in AAM82170 to AAM81921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) consists and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For the activity of (I) by expression in a patient's genome cathat affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the correct of (I) proteins and polynucleotides may be used to produce the secreted (I). by inserting the nucleic acids into a host cell and culturing the cell to express the correct of (I) proteins and polynucleotides may be used to prevent, (I) cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8794 represent human immune/haematopoietic-derived cells. AAK64703 corepresent sequences used in the exemplification of the present invention.
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                                                                    ACTTCCAGGAATGTCACACGATGAAATATCTCTGCTGAAGACAGTGGATAAAAAAACAG
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17-NOV-2000;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially access to the control of the control of the cell of the control of the cell of th
                                                                                                                                                                                                                                                                                                                                                        cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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    TAGCAACCCTTGCAATGAAGATGAGCAGATCCACAGGAAAACTTGAATGCACAACTGTCT
                                               AACTGTCTTTGACAGTGAGAAAAATATTCAGAATAACCATATCCCTGTGCCGTTATTACC
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02-MAR-2000;
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2000US-0199076
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         CC antino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) CC artivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC supplement the patients own production of (I). Additionally, (I) cc polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoletic-derived cells. AAK64703 cc sequences from the present human immune/haematopoletic antigen genomic conservations. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic
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17 - NOV - 2000
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P-PSDB;
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17-NOV-2000;
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DB; AAM89038.
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                                                                                                                                                                                                                                                                                                                     human immune/hematopoietic antigen diagnosing and/or treating cancers
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Best Local
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29-MAR-1999;
24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                            immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Digeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; atomacompatibility class II deficiency disease; and company disease; atomacompatibility class II deficiency disease; atomacompatibility disease; atomacomp
                                                                                                                                                                                                                                                                                                                                                                                       immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; gene therapy; B cell associated immune system disorder; food allergy;
                                                                                                                                 05-OCT-2000
                                                                                                                                                                                                                        Homo
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                                                                                      28-MAR-2000;
                                                                                                                                                                             WC200058480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activation-induced cytidine deaminase; AID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human activation-induced cytidine deaminase exon 3 SEQ
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                                                                                      2000WO-JP01918
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99JP-0087192.
99JP-0178999.
99JP-0371382.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytidine deaminase
                                                                                                                                                                                                                                                               disease;
selection
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RESULT 9
AAC55316
ID AAC55
XX
AC AAC5
XX
DT 05-F
DT 05-F
DX
DX
LIMBUR
KW ACTI
KW ACTI
KW anti

05-FEB-2001

(first

entry)

AAC55316

standard;

DNA;

148 ВP

241

GGGGTGCAAATAGCCATCATGACCTTCAAAG

Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatol gene therapy; B cell associated immune system disorder; food all

dermatological; food allergy;

activation-induced cytidine deaminase exon

N

SEQ

B

NO:12

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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 271
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 271 BP; 47 A; 95 C; 76 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN
(HONJ/) HONJO
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                                                  CATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC
                                                                                                                                                                                         GGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGA
                                                                                                                                                                                                           GGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGA
                                                                                                                                                                                                                                                              AACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCT
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                  Score 271; DB 21;
Pred. No. 2.9e-93;
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                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       53 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  0
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Gaps

0

415

120 355 60

240 475 180

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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and Cd dermatological activities, and can be used in gene therapy. AID CD polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (JgA) deficiency Cd diseases, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen Cd disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgC discriber, and IgG subclass selection disorder. The DNA sequences cencoding AID may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The DNA sequence of human AID.
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-1999;
24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 150;
                                                                                                                                                                                                                                                                                 Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-611715/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2000; 2000WO-JP01918
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121
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HONJO
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t for drug deve
              ACTGGACTTTGGTTATCTTCGCAATAAG
                                                                                   TCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTC
                                                                                                                                     , CCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGGCTGGGCTAAGGG
                                                                                                                                                            CCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGG
                                                                 TCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTC
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                 B₽;
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99JP-0178999.
99JP-0371382.
                                                                                                                                                                                                                                                                               35 A; 33 C; 38 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development
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                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation induced cytidine deaminase, useful elopment for immune-related diseases including
                                                                                                                                                                                                            0;
                                                                                                                                                                                                                              Score 148;
Pred. No.
                                                                                                                                                                                                            Mismatches
                              235
                                                                                                                                                                                                                              1.5e-46;
                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                           Length 148;
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RESULT 10 AAC55315 ID AAC55 XX

AAC55315

standard; DNA;

87

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61

87

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                                                                                                                                                                                                       The present invention describes an activation-induced cytidine deaminase (C (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and C has cytidine activity similar to APOBEC-1. AID has antiallergic, C antianaemic, antiasthmatic, ophthalmological, anti-HIV and C dermatological activities, and can be used in gene therapy. AID C polypuclootides are useful in methods for identifying drugs for the C treatment of B cell associated immune system disorders, immunodeficiency C diseases and allergies, such as immunoglobulin A (IgA) deficiency C diseases, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen C disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen C colltis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen C immunodeficiency disease, ataxia telangiectasia, common variable C immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated C IgE disorder, and IgG subclass selection disorder. The DNA sequences C encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The
                                                                                                                        Query Match
Best Local S
Matches 87
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthmatigh nephritis; gamma-globulinaemia; atopic dermattitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease;
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 150; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid
a target for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-611715/58
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(HONJ/) HONJO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency syndrome; IgG subclass selection disorder;
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                                                              AGAGAACCATCATTAAITGAAGTGAGAITTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGA
                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding activation induced cytidine deaminase,
for drug development for immune-related diseases in
    AGACACTCTGGACACCACTATGGACAG
                                       AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muramatsu
                                                                                                                          Conservative
                                                                                                                                                                                                       BP; 28
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99JP-0178999.
99JP-0371382.
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100.0%;
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                                                                                                                          0;
                                                                                                                                        Score 87;
Pred. No.
                                                                                                                                                                                                  23 G; 19 T; 0 other;
                                                                                                                        Mismatches
                                                                                                                                             No.
                                                                                                                      2.2e-23;
hes 0;
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                                                                                                                                                           Length 87
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                                                                                                                        Gaps
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RESULT 11
AAC55313
      29-MAR-1999;
24-JUN-1999;
27-DEC-1999;
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                                  disease, IgA nephritis, gamma-globulināemia, atopic dermatitis, allergi colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AII protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the polynucleotides are useful in methods for identifying drugs for the
                                                                                                                                                                                                         treatment of B cell associated immune system disorders, immunodefi diseases and allergies, such as immunoglobulin A (IgA) deficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (/CNJ/)
                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 142-145; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611715/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Honjo T, Muramatsu
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HONJO
  5514 BP;
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99JP-0178999.
99JP-0371382.
1709 A; 1045 C; 1134
  G; 1623 T; 3 other;
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                                  these disorders. The of human ATD
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AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGA

Matches

87;

Conservative

0 Score | Pred.

Mismatches No.

Similarity

3.1%;

DВ 1.2e-23; 21;

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                                                                                antianaemic, antiasthmatic, ophthalmological, anti-HTV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IGA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic trinitis, Rosen disease, Dideorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological, anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; 13A nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Discorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease;
                                                 encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The
                                                                                                                                                                                                                                                                                (AID). AID structurally relates to an RNA editing enzyme APOBEChas cytidine activity similar to APOBEC-1. AID has antiallergic,
                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 151; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including
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                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to cupplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic concerns the present invention. AAK54920 and AAK84950 and AA
                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                               53
                                                                                                                                                     Score 74;
Pred. No.
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                                                                                                                                          Mismatches
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                                                                                                                                                     DB 22;
1.6e-18;
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                                                                                                                                                                                                other;
                                                                                                                                        0;
                                                                                                                                                                  Length 280
                                                                                                                                        Indels
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RESULT 15
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RESULT 14 ABV22611/c

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ABV28433

standard; cDNA;

481

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Query Match
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Matches 70
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25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                          Sequence 481
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                                                                                                                                                                                                                                                                                                                     patient;
(I) is also
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(f) assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (d) assessing the efficacy of a therapy
in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patie assessing the prostate call carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient determining whether prostate cancer in a setient assessing the aggressiveness or indolence of prostate cancer in a
                                             2046
144
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                                             AGGTTGCAGT
                                                                                        CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG
                                                                                                                                  CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG
AGGTTGCAGT
                                                                                                                                                                                                                                                                                                                  useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                2.5%;
ilarity 100.0%;
Conservative (
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2000US-189862P
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gene; ss.
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                                                                                                                                                                                score 70; DB Pred. No. 4.8
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                                                                                                                                                                                                                                                                          153 T; 3 other;
                                                                                                                                                                                                     DB 23;
4.8e-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibiting prostate cancer
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 5931; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                      Sequence 481 BP; 111 A; 103 C; 111 G; 153 T; 3 other;
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                                                                                                                                                                                                                   is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                   selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                2046 AGGTTGCAGT 2055
                                                                                       1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 2045
144
                                                               204
                                                                                                                                         2.5%;
Similarity 100.0%;
                                                         CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG
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; 2000US-189862P.
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; 2000US-2119107P.
; 2000US-255281P.
                                                                                                                            Conservative
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                                                                                                                            0,
                                                                                                                                           Score 70;
Pred. No.
                                                                                                                          Mismatches
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                                                                                                                                         4.8e-17;
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                                                                                                                                                        Length 481
                                                                                                                        Indels
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Search completed: July 7, 2003, 20:19:18 Job time : 613 secs

Appli Appli

18. Appli
5. Appli
7. Appli

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Post-processing: Listing first 45 summaries
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seq length: 2000000000
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2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-798-096-10
US-09-797-906-3
US-09-797-906-3
US-09-345-882-1
US-08-909-965C-4
US-08-909-965C-4
US-09-404-879A-136
US-09-404-879A-3
US-09-404-879A-3
US-09-404-879A-3
US-09-167-681-29
US-08-781-891-79
US-09-781-211-3
US-09-613-444-1
US-09-613-444-1
US-09-613-444-1
US-09-167-681-37
US-09-749-588-3
US-09-348-673-83
US-08-450-6352-3120
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US-08-345-217-3
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US-09-798-096-10/c
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                                                                                                                                                                                                                                                     Sequence 3, Application US/09797906
Patent No. 6329188
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001151CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: GENERAL INFORMATION: Ward APPLICANT: Donna T. Ward APPLICANT: Donna T. Wart TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
TYPE: DNA
TYPE: DNA
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Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                    SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
NAME/KEY: misc_feature
LOCATION: (1)...(84495
OTHER INFORMATION: n =
                                                                ORGANISM: Human FEATURE:
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                                                                                                            TYPE: DNA
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US-09-780-049-18
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US-08-814-095-7
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US-09-426-290-1
US-08-480-784-3
US-09-641-638-350
US-08-480-784-20
US-08-483-553-20
US-08-483-553-20
US-08-488-0118-20
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Best Local Similarity
Matches 57; Conserv
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A
TITLE OF INVENTION: AND POLYMORPHIC MARKERS A
FILE REFERENCE: GENSET 031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEI, Ming-Hui et al TITLE OF INVENTION: IROCATED HUMAN PHOSPHODIESTERASE TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF FILE REFERENCE: CL001063
CURRENT EPPLICATION NUMBER: US/09/754,250
CURRENT FILING DATE: 2001-01-05
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30
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SOFTWARE: FastSEQ for
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TYPE: DNA
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LOCATION: (1)...(111282)
OTHER INFORMATION: n = A
 LOCATION: 88073 OTHER INFORMATION:
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LOCATION: 72794
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FEATURE:
NAME/KEY: allele
               NAME/KEY: allele LOCATION: 103783.
                                                  LOCATION: 99094..99
OTHER INFORMATION:
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LOCATION: 99094..99140
                                                                                                                                                     NAME/KEY: allele
LOCATION: 99075..99
OTHER INFORMATION:
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LOCATION: 88050..88096
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LOCATION: 90819..90
OTHER INFORMATION:
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LOCATION: 72771...
                                                                           NAME/KEY: allele
                                                                                                    OTHER INFORMATION:
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LOCATION: 99075.
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LOCATION: 72771..72817
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LOCATION: 97130..97177
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LOCATION: 97099..97145
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LOCATION: 97099..97145
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LOCATION: 93690..
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LOCATION: 160031
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fragment 5-131-395
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US-08-909-965C-4
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Best Local
                                                                                                                                CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
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LOCATION: 108127...1
OTHER INFORMATION:
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LOCATION: 108127.,108177
OTHER INFORMATION: polymorphic
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LOCATION: 106918...1
OTHER INFORMATION:
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LOCATION: 108084
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LOCATION: 108084
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                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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        APPLICATION NUMBER: JP 322745/95
APPLICATION NUMBER: PCT/JP96/03630
FILING DATE: 12-No. 5936078-1995
FILING DATE: 12-Dec-1996
                                                                                           APPLICATION NUMBER: FILING DATE: August
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VENTION: NOVEL DNA,
VENTION: AND NOVEL
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Zhao Nanding
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ON: 514
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; FEATURE:

NAME/KEY: misc_feature

; LOCATION: (1)...(176373)

; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-17
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                                                             RESULT 7
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Sequence 136, Application Patent No. 6468546 GENERAL INFORMATION:
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Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
CURRENT FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/094,646
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          LENGTH: 176373
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ORIGINAL SOURCE:
ORGANISM: hum
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                                                                                                    1990 TAATCCCAGCTACTTGGGAGGCTGAGGCAGAAATCGCTTGAACCCAGGAGG 2042
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l Similarity 100.0%;
53; Conservative 0;
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55; Conserv
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DEDNESS: double
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to 829
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                              US/09404879A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB red. No. 1.1.0; Mismatches
                                                                                                                                                                                 Score 53;
Pred. No.
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 2; Le
o. 1.1e-12;
tches 0;
                                                                                                                                                                                DB 3; Le
3.1e-12;
                                                                                                                                                                                                Length 176373;
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                                                                                                                                                                  Indels
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46202
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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US-09-404-879A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for SEQ ID NO 1
LENGTH: 461
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-404-879A-136
                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09404879A
; Patent No. 6468546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 136
LENGTH: 341
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.08;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09404879A Patent No. 6468546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 1.8%; Score 52; DB 4; Length 461; Local Similarity 100.0%; Pred. No. 1.8e-11; hes 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1829 GGGCCGGGGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAG 1880
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TYPE: DNA

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US-09-167-681-29/c
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Best Local Similarity
Matches 52; Conserv
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Best Local
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 7152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weinshilboum, I
APPLICANT: Raftogianis, R
APPLICANT: Wood, Thomas C
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/167,681A CURRENT FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Otterness, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (3810)...(3956)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAME/KEY
                                                              TITLE OF INVENTION:
                            CORRESPONDENCE ADDRESS
                                                                                            APPLICANT:
                                                                                                         APPLICANT:
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                                                                                                                                           APPLICANT:
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                                                NUMBER OF SEQUENCES:
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                1991 AATCCCAGCTACCTTGGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGG 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1829 GGGCCGGGCGTGGTGACGCCTGTAATCCCAGCACTTTGGGAGGCCGAG 1880
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                                                                                                                                                                                                                                                                                                                                              52;
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                                                                                                                      Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
E: SEED and BERRY LLP 6300 Columbia Center,
                                                           Schellenberg, Gerald D.
VENTION: GENE AND GENE PRODUCTS RELATED TO
VENTION: WERNER'S SYNDROME
                                                                                                        Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                           1.8%; Score 52; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                            Mismatches
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 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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1.8e-11
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                                                                                                                                                                                                                                                                                                                                                                      Length 7152;
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US-09-791-211-3/c
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Best Local Simi
                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 87543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                        NAME/KEY: unsure
LOCATION: 12742
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29370
                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: unsure
LOCATION: 7421
            OTHER INFORMATION: unknown
                                                                                                                                                                                                                NAME/KEY: unsure LOCATION: 7427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Sequence 3, Application US/09791211 Patent No. 6448080
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS 0205
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Donna T
APPLICANT: Andrew 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                     OTHER INFORMATION: unknown
                                                                                                                                                                             OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,3:
REFERENCE/DOCKET NUMBER: 39,3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78531 GCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTT 78480
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79:
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NAME/KEY: unsure LOCATION: 30136 OTHER INFORMATION: L

unknown

AMME/KEY: unsure LOCATION: 29981

THER INFORMATION:

unknown

OTHER INFORMATION: unknown

OTHER INFORMATION: unknown

COCATION: 29422 OTHER INFORMATION:

unknown

VAME/KEY: unsure LOCATION: 31205 OTHER INFORMATION: unknown

OCATION: 30140 THER INFORMATION:

unknown

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В
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                                                                                                                                                                                                                                                                              US-09-078-294-9/c
                                                                                                                                                                                                                                                                                                RESULT 13
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Best Local S
Matches 52
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                            Seguence 9, Application US/09078294 Patent No. 6265211
                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
                                                                                                                                   APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                 CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
                                                                                      NUMBER OF SEQ ID NOS: 29
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OTHER INFORMATION: unknown
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LOCATION: 68739
OTHER INFORMATION: unknown
ORGANISM: BAC-F2 contig
                   TYPE:
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OTHER INFORMATION: unknown
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LOCATION: 79134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure LOCATION: 69785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure LOCATION: 68733
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OTHER INFORMATION: unknown
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LOCATION: 63290
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                                ENGTH: 1701
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                                                                                                                                                                                                                                                                                                                                                 ch 1.8%; Score 52; DB 1 Similarity 100.0%; Pred. No. 8: 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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8.3e-12;
hes 0;
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NAME/KEY: unsure
LOCATION: 34066
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34072
OTHER INFORMATION: unknown

AME/KEY: unsure OCATION: 39020 THER INFORMATION: unknown

AME/KEY: unsure OCATION: 36816 THER INFORMATION: unknown NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33160
OTHER INFORMATION: unknown

NAME/KEY: unsure OCATION: 31592 WIHER INFORMATION: unknown

OCATION: 31206 THER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 52787 OTHER INFORMATION: unknown NAME/KEY: unsure LOCATION: 53384

NAME/KEY: unsure LOCATION: 52786 OTHER INFORMATION:

unknown

NAME/KEY: unsure LOCATION: 47291 OTHER INFORMATION: unknown

NAME/KEY: unsure LOCATION: 46826 DTHER INFORMATION: unknown

OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown

AME/KEY: unsure OCATION: 42459 THER INFORMATION: unknown

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AME/KEY: unsure OCATION: 42164 THER INFORMATION:

unknown

US-09-078-294-9

Query Match 1.8%; Score 51; DB 4; Length 1701; Best Local Similarity 100.0%; Pred. No. 3.7e-11; Matches 51; Conservative 0; Mismatches 0; Indels

0, Gaps

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FILE OF INVESTION. DESCRIPTION OF THE REFERENCE: PENN-0731
CURRENT APPLICATION NUMBER: US/09/689,423
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/195,620
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 199-10-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 3844
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. 6414131
GRMERAL INFORMATION:
APPLICANT: Berrettini, Wade H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/613,444
CURRENT FILING DATE: 2000-07-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Ludwig, Erwin H.

APPLICANT: Farese, Robert V.

APPLICANT: Forese, Robert V.

APPLICANT: Cases, Sylvaine

TITLE OF INVENTION: Polymorphisms in a Diacylglycerol

TITLE OF INVENTION: Acyltransferase Gene, and Methods of Use Thereof.

FILE REFERENCE: 6510191081
                                                                                    Matches
                                                                                                   Query Match 1.8%; Score 51; DB 4; Best Local Similarity 100.0%; Pred. No. 3.2e-11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berrettini, Wade H.
TITLE OF INVENTION: Gene and Methods for Diagnosing Neuropsychiatric
TITLE OF INVENTION: Disorders and Treating Such Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 51; DB 4; Length 2174; Local Similarity 100.0%; Pred. No. 3.5e-11; ses 51; Conservative 0. Micmatal.
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                     1986 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCC 2036
                                                                                    Conservative
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Search completed: July 7, 2003, 23:19:41 Job time: 160 secs

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Minimum
Maximum
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length: 2000000000
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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11204
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1.18 9 US-09-966-880A-7
64 9 US-09-966-880A-15
70 9 US-09-966-880A-15
71 9 US-09-966-880A-13
72 9 US-09-966-880A-13
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               Sequence 7, Appli
Sequence 10, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 9, Appli
Sequence 281, Appl
Sequence 273, App
Sequence 922, App
Sequence 923, App
Sequence 1366, Ap
Sequence 3365, Ap
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US-09-764-891-9613	US-09-764-847-1253 US-09-954-456-1146 US-09-764-891-19186 US-09-764-891-10186	US-09-764-897-2653 US-09-764-877-2653 US-09-918-995-25881 US-10-060-036-3361 US-10-092-154-1253	US-10-072-349-295 US-10-072-349-295 US-10-0764-855-295 US-10-072-349-992 US-09-764-855-292 US-09-898-556A-10 US-09-811-469-3 US-09-880-107-1543 US-09-880-107-1543 US-10-09-154-1975	US-09-764-891-7619 US-09-920-671-11 US-09-764-877-3810 US-10-991-504-1475 US-10-764-869-1475
Sequence 3234, Appli Sequence 9613, Ap	Sequence 123, Ap Sequence 1146, Ap Sequence 8995, Ap Sequence 10186, A	Sequence 6037, Ap Sequence 2653, Ap Sequence 25881, Ap Sequence 3361, Ap Sequence 1253, Ap	Sequence 295, App Sequence 295, App Sequence 292, App Sequence 292, App Sequence 10, Appli Sequence 3, Appli Sequence 1543, Ap Sequence 1975, Ap	Sequence 7619, Ap Sequence 11, Appl Sequence 3810, Ap Sequence 1475, Ap Sequence 1475, Ap

ALIGNMENTS

US-09-966-880A-7

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; NAME/KEY: 3'UTR; LOCATION: (677)...(2818) US-09-966-880A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09966880A Patent No. US20020164743A1
Query Match
Best Local Similarity
Matches 2818; Conserv
                                                                                                                                                                                                                                                                                                      SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR FILING DATE: 1999-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                        FEATURE:
                                                                                                                                       NAME/KEY: 5'UTR
LOCATION: (1)...(79)
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LOCATION: (80)...(673)
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Pred. No. 0;
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1 AGAGAACCATCATTAATTGAAGTGAGAFTTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGA 60

Db Db Db

1081 AGTGGTGTTAGTGATAGATTTTTCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACAC 11 	21 GTGAGAGGATCAAATGTTTTTATATCAACATCCTTTATTATTTGAGTTCATTTGAGTTAAC 1 		901 GCAACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGT 960	9 9	781 TITCTTAGAGTTTACAGAAAAAATATTTATATAGAACTCTTTAAAAAGATCTATGTCTTG 84	7 7	7	0 0	541 CCATGAAAGACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCCAG 6	10 10		361 GGCCGACTITCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTA 420	CTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGT	241 CTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCG 300	181 GAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGG 24	121 ATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGACCTACCT	1 AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGA 60 61 AGACACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCA 12
40 Oy 40 Db		O Db	. Oy	00 Db	O DD DV	O Db	20 Qy 20 Db	60 Ad Ad	00 dd Qy		Qy	Qy Db	Q dd	Qy	O Db	ДУ	Db Qy
2161 GGAGAGGATGGGGAAGCAATTCCAAGGAAATTGTGCTTTATCCAACAAAATTGTAAGGA 2220 	101 AGACTCTGTCTCAGAAAAAAAAAAAAAAAAAGAGAGAGAG	2041 GGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCA 2100		921 GGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGC 	861 CAGCACTTTGGGAGCCCGACCCGGCGGATCACCTGTGGTCAGGACTTTGAGACCAGCCT 	801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1741 TGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGCCACATAACAAGATCCTGTCTCTCAA 1800 	681 A	621 GATGCTTCTCCCAAAGGTATATTAACTATATAAGAGAGATTGTGACAAAACAGAATGATAA 	61 GGGTCTCTTCATCTCAGAAATGCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGT 	01 GCAAACAATTGGAAGGAAGTTGCTTGAATGTTGGGGAGAGGAAAATCTATTGGCTCTCGT 	441 AAACTOTTTTAAGGAAGTOCOTAATTTAGAAACACCCACAAACTTCACATATCATAATTA 15 	381 TGTGAACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGC 	1321 GACCATGCATGCTCAACCTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGAC 1380 	261 CAGAAGCATGTTTTATGTTTGTACAAAAGAAGATTGTTATGGGTGGG	201 GACCCCAAACCATCTCTCCAAAGCATTAATATCCAATCATGGGCTGTATGTTTTAATCAG -	141 AAACTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGT

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NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.

SEQ ID NO 35

LENGTH: 11204

TYPE: DNA
ORGANISM: Homo sapiens
US-09-966-880A-35
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APPLICANT: Honjo, Tasuku

APPLICANT: MUTAMATSU, MASAMICHI

TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE

FILE REFERENCE: 06501-088001

CURRENT APPLICATION NUMBER: US/09/966,880A

CURRENT EILING DATE: 2001-09-28

PRIOR FILLING DATE: 2000-03-28

PRIOR FILLING DATE: 1090-12-27

PRIOR APPLICATION NUMBER: JP 11-371382

PRIOR APPLICATION NUMBER: JP 11-371382

PRIOR FILLING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: JP 11-17899

PRIOR FILLING DATE: 1999-06-24

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                               ATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTCTCCAA 1221
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                                    GTCTCTTTTGGTGTCTATTTGTCCCTAACAACTGTCTTTGACAGTGAGAAAAATATTCAG
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CURRENT FILING DATE: 2001-09-28
PRIOR REPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR PELICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SED ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 2172
TYPE: DNA
ORGANISM: Home sapiens
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                                                                                                                          Matches
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723 TACCAATAAAA 	Db Db	1643 TAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGC 1702 	dd VQ
2663 2041	Оу	1583 CCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGTGT	Qy Db
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2543 AATTTATAACTTTAGAAATGATTCTAATAACAACCTATGTAATTCTAACASTTGCAGTAAT	ОУ	1463 AATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAAAACAATTGGAAGGAA	Qy Db
2483 ATTTTTATTAACATGATTTOCTTTTCTGATATTGAAATGGAGTCTCAAAGCTTCATA	Оу	1403 TGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCCT 1462 	Qy Db
2423 AGAGTTAAAAAFTGTTACTTCATGTATTCATTTATATTTATATTTTGCGTCTAATG 2482 	da Qy	1343 GCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCCTAATAA 1402 	Qу ДЪ
2363 ACAGGAAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTTTGTAAA	QQ QY	1283 TACAAAAGAATGTTATGGGTGGGGGATGGAGGTATAGACCATGCATG	ОУ
2303 ATRACCATATCCCTGTGCCGTTATTACCTACCACCCTTGCAATGAAGATGAGCAATCC 	ДУ	1223 GCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAGAAGCATGTTTTTATGTTTG 1282	dd Vy
2243 TCTCTTTTGGTGTCTATTTGTCCCTAACAACTGTCTTTGACAGTGAGAAAAAATATTCAGA	Db V9	1163 TCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTCTCCAAA 1222 	ОУ
2183 TGCAAGGAAATTGTGCCTTATCCAACAAAATGTAAGGAGCCAATAAGGGATCCCTATTTG	, pp %	1103 TCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACACAAACTCTTCCATCAGGCCATGA 1162	ОУ
2123 AAAAAAAAGAGAGAGAGAGAAGAAACAATATTTGGGAAGAAGAATGAGGAAGCAT	da VY	1043 TATCAACATCCTTTATTATTTGATTCATTTGAGTTAACAGTGGTGATAGTGATAGATTTT 1102 	Qy Db
2063 1441	Db	983 GGTAGGATGAGAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATGTTTTTA 1042 	Qy Db
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1943 1321	Db	863 CTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCCCTACTGGGA 922 	QУ
1261	Db	803 ATATITATATAGACTOTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGGAAGGAA	Qу
1201	Db S	743 CCTTCAAGTCTTCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTACAGAAAA 802 	Qy Qy
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PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 148
TYPE: DNA
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PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
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Best Local
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APPLICANT: MUTAMATSU, MESAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINA:
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
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TITLE OF INVENTION: NOVEL CYTIDI
FILE REFERENCE: 06501-088001
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ORGANISM: Homo sapiens
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Conservative (
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                                                                                                                                                                                                                            RESULT 8
US-09-966-880A-9
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Best Local (
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Best Local :
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Sequence 9, Application US/09966880A

Patent No. US20020164743A1

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: MURAMATION:
TITLE OF INVENTION: MOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
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APPLICANT: Honjo, Tasuku
APPLICANT: MUTAMATSU, MAGAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
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Patent No. US20020164743A1
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PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR EILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR RILING DATE: 1999-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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148; Conserv
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87; Conserv
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Pred. No.
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                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HOJO, TASUKU
APPLICANT: MUTAMATSH, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/966,880A CURRENT FILING DATE: 2001-09-28
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PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36
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                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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NAME/KEY: intron
LOCATION: (1)...(1031)
FEATURE:
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LOCATION: (1119)
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LOCATION: (1032)...(1118)
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                                                                                                                                                     Match 2.8%; Score 78; Local Similarity 100.0%; Pred. No.
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605 CTTCGGCGCATCCTTTTG 622
                                                       39 GAAAGAACTTTCAAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                            NUMBER: JP 11-87192
1999-03-29
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o. 7.6e-29;
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. 3.2e-33;
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                                                                              Best Loc
Matches
                                                                                                                                                                                                                                              SOFTWARE: Pa
SEQ ID NO 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020102531A1 GENERAL INFORMATION:
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LENGTH: 167343
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                                                                                                                       Query Match
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/80/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTMARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign TITLE OF INVENTION: Sets FILE REFERENCE: 689290-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Horrigan,
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 583
                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                             LENGTH: 167343
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131153 CCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGG 131094
                                                                                                  Local
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                                                                            1 Similarity
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RESULT 12
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PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1
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PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
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CURRENT FILING DATE: 2002-02-14
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OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: 60/234,274
OR FILING DATE: 2000-09-21
OR APPLICATION NUMBER: 60/234,223
OR FILING DATE: 2000-09-21
OR APPLICATION NUMBER: 60/228,924
OR APPLICATION NUMBER: 60/228,924
OR FILING DATE: 2000-08-30
OR APPLICATION NUMBER: 60/224,518
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OR FILING DATE: 2000-08-22
OR APPLICATION NUMBER: 60/216,647
OR APPLICATION NUMBER: 60/225,267
OR FILING DATE: 2000-07-07
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/216,880
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/225,270
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OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/218,290
OR FILING DATE: 2000-07-14
OR APPLICATION NUMBER: 60/225,757
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OR FILING DATE: 2000-08-14
                                                                                DR APPLICATION NUMBER: 60/220,964
DR FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/241,809
DR FILING DATE: 2000-10-20
DR APPLICATION NUMBER: 60/249,299
DR FILING DATE: 2000-11-17
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   APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
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Query Match
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OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/231,242
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/232,081
OR APPLICATION NUMBER: 60/232,080
OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/231,414
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OR APPLICATION NUMBER: 60/231,244
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OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,215
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APPLICATION NUMBER: 60/249,207
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APPLICATION NUMBER: 60/241,826
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US-10-074-095-923
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; Publication No. U
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PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR PELICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR PRIOR PELICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PELICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PRIOR DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
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FILING DATE: 2000-10-20
REILING DATE: 2000-11-20
REPLICATION NUMBER: 60/249,299
REPLICATION NUMBER: 60/236,327
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ETILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
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o. US20030077704A1
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                                                        60/244,617
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OR APPLICATION NUMBER: 60/229,345
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,287
OR TILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/229,513
OR FILING DATE: 2000-09-05
OR APPLICATION NUMBER: 60/231,413
OR FILING DATE: 2000-09-08

APPLICATION NUMBER: 60/229,343 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/234,997 FILING DATE: 2000-09-25

APPLICATION NUMBER: 60/251,868 FILING DATE: 2000-12-08 APPLICATION NUMBER: 60/229,344 FILING DATE: 2000-09-01

APPLICATION NUMBER: 60/251,856 FILING DATE: 2000-12-08

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60/236,368

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NUMBER: 60/236,367

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60/237,038

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APPLICATION NUMBER: 60/237,039

FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/236,802
FILING DATE: 2000-10-02

APPLICATION NUMBER: 60/237,037 FILING DATE: 2000-10-02

APPLICATION NUMBER: 60/240,960 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/237,040 FILING DATE: 2000-10-02

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PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,414

PRIOR FILING NUMBER: 60/231,414
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APPLICATION NUMBER: 60/249,213
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/232,081
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APPLICATION NUMBER: 60/232,400
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APPLICATION NUMBER: 60/249,264
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FILING DATE: 2000-11-17
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FILING DATE: 2000-10-20
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Pred. No. 8.8e-23;
); Mismatches 0;
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OR APPLICATION NUMBER: 60/239,935
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/239,937
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/241,787
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/246,532
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/249,216
OR APPLICATION NUMBER: 60/249,216
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,210
OR APPLICATION NUMBER: 60/249,210
OR APPLICATION NUMBER: 60/226,681

APPLICATION NUMBER: 60/249,218 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,208

APPLICATION NUMBER: 60/ FILING DATE: 2000-06-30

60/215,135

60/225,266

APPLICATION NUMBER: 60/ FILING DATE: 2000-09-06

APPLICATION NUMBER: 60/ FILING DATE: 2000-08-14

APPLICATION NUMBER: FILING DATE: 2000-0 APPLICATION NUMBER: 6 FILING DATE: 2000-08-

2000-09-

60/235,836 60/230,438

60/225,214

APPLICATION NUMBER: 60/227,182 FILING DATE: 2000-08-22

APPLICATION NUMBER: 60/ FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/ FILING DATE: 2000-08-14

60/225,759 60/225,213

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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 922
LENGTH: 125
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-860-922
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 923
LENGTH: 125
TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: July 7, 2003, 23:28:03 Job time: 493 secs
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Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
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CZGO/MAR	AAM58174	ABB22810	ABB37512	ABB32258	AAU50497	AAW30763	ABB61050	AAB24197	AAB24198	ij	SUMMARIES
Human bone marrow	Human brain expres	Protein #4809 enco	Peptide #5018 enco	Peptide #4909 enco	Propionibacterium	Mannose-1-phosphat	Drosophila melanog	Mouse activation-i	Human activation-i	Description	ES

29-MAR-1999; 24-JUN-1999; 27-DEC-1999;

99JP-0087192. 99JP-0178999. 99JP-0371382.

05-OCT-2000

WO200058480-A1

28-MAR-2000; 2000WO-JP01918

7 3 5 294 22 ABB12440 Huma	7 3.5 287 21 AAG59641 Arak	7 3.5 286 21 AAG04861 Arab	7 3.5 272 22 AAU23799 Nove	7 3.5 263 21 AAG60326 Aral	7 3.5 263 21 AAG53070 Aral	7 3.5 262 21 AAG52430 Aral	7 3.5 259 21 AAG53107 Aral	7 3.5 259 21 AAG17740	7 3.5 257 21 AAG60333	7 3.5 243 18 AAW55254	7 3.5 240 21 AAG53071	7 3.5 239 21 AAG52431	7 3.5 236 21 AAG53108	7 3.5 236 21 AAG17741	7 3.5 222 22 AAU23537	7 3.5 222 21 AAB57	7 3.5 221 22 AAM40691	7 3.5 220 21 AAG59642	7 3.5 210 22 AAU23550	7 3.5 196 21 AAG60327	7 3.5 190 23 ABB48789	7 3.5 190 22 AAM38905	7 3.5 190 21 AAG59354	7 3.5 190 21 AAB11	7 3.5 190 19 AAW77092	7 3.5 188 23 ABP06725	7 3.5 188 21 AAB41276	7 3.5 163 23 ABB97879 Human	7 3.5 132 21 AAG59355 Arabi	7 3.5 131 22 AAU31332	7 .3.5 114 19 AAW54390 Acti	7 3.5 80 22 AAM82	0337 Huma	7 3.5 54 22 AAM18471 Pepti
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ALIGNMENTS

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Human activation-induced cytidine deaminase SEQ ID NO:8
                                                                                 05-FEB-2001
                                                                                       AAB24198;
                                                                                             AAB24198 standard; Protein;
                                                                                 (first entry)
                                                                                              198
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immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system discorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IçA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergic rhinitis; Rosen disease; Bigeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto Homo sapiens Activation-induced cytidine deaminase; AID; immunodeficiency syndrome; IgG subclass selection disorder. cytidine deaminase;

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RESULT 2
AAB24197
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AC AAB2
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XX O5-F
XX Mous
XX Mous
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        immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritts; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy drug allergy, allergic rhinitis, Rosen disease, Digeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 140-141; 174pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding activation induced cytidine deaminas a target for drug development for immune-related diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Honjo T,
                                                                                                             Activation-induced cytidine deaminase; AID; cytidine deaminase;
                                                                                                                                      Mouse activation-induced cytidine deaminase SEQ ID NO:2.
                                                                                                                                                                                                    AAB24197;
                                                                                                                                                                                                                              AAB24197
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histocompatibility class II deficiency disease;
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HONJO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                              standard;
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                              Protein;
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Pred. No. 2.6e-192;
; Mismatches 0;
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diseases including
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27-DEC-1999;
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                                       Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                           Similarity 42; Conserv
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HONJO
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(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and that cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, Difeorge disease, MHC (major histocompatibility class) class immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
Drosophila; developmental biology; cell signalling; insecticide;
                                                            Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse activation-induced cytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 131-132; 174pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     auto immunodeficiency syndrome; IgG subclass selection disorder
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99JP-0178999.
99JP-0371382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB577737-ABB72072).
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Positive regulatory gene of mannose-1-phosphate useful for high mannose type neutral saccharide
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02-JUN-2000;
07-JUL-2000;
sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogeni polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by placenes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Placenes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of Placenes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for Placenes proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomy uveitis; endophthalmitis; bone; joint; central nervous system; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is encoded by the gene of the invention, designated MNN4, and is a protein which positively regulates mannose-1-phosphate transfer in yeast. The gene is useful for the preparation of human high
                                                                                                                                                                                                                                    Propionibacterium acnes vaccinating against and treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                      Skeiky
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30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypertosis; osteomyelitis;
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RESULT 6
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Best Local S
Matches 7
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26-MAY-2000;
30-JUN-2000;
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      downregulate expression and activity of P. acnes polypeptides therefore treat P. acnes infections. The antibodies may also be diagnostic agents for determining P. acnes presence, for example 1.1kked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                  Claim 27;
                                                                                                                                                                                                                                                                                                                                                           breast,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #4909 encoded by breast cell single exon nucleic acid probe
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                                                                                                                                                                                                                                                                                                                                                     spatially-addressable set of single exon nucleic acid pr
ful for measuring gene expression in sample derived from
ast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
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                                                                                                                                                                                                                                                                                                                  SEQ
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                  NO 15226;
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                                                                                                                                                                                                                                                                                                              327pp + sequence listing; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
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22;
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Score 7; I

DB 23; 22;

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Sequence

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RESULT 7
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26-MAY-2000; 2000US-0207456
30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rapid production of functional information from genomic present sequence is a peptide encoded by a single exonorobe of the invention.

Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single excountly make the five fitter that the invention.
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04-OCT-2000;
                                   printed
                                             Note:
                                                                                                                                    Claim
                                                                                                                                                         analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
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                     :rom WIPO
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                                The sequence data for this patent did not form part specification, but was obtained in electronic form
                                                                                                                                     27;
                                                                                                                                                          genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                          foetal liver; gene expression;
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                      at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                    listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                    English
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                                   format directly
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                       measuring human gene expression in a sample derived from human heart (se ABA21535-ABA41305). The present sequence is a protein encoded by one suc probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease.
                                                                                                                        hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                    Single
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                         Sequence
                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                    Claim 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein #4809 encoded by probe
                                           Local Similarity les 7; Conserv
                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                     IMTFKDY 144
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IMTFKDY 12
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; 2000US-0632366.
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2000US-0207456.
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                                                      Score 7; DB 22; Pred. No. 23;
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                                            Mismatches
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RESULT 9
AAM58174
ID AAM5

AAM58174 standard; Protein; 54 AA.

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PN XXX XXX ACC
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single
brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which may enable the diagnosis and improved treatment of r diseases such as Alzheimer's disease, multiple sclerosis, epilepsy and cancers. The present sequence is a protein er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
WO200157276-A2
                                             Homo sapiens.
                                                                                                                                                                      Human
                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                     AAM70625;
                                                                                                                                                                                                                                                                                                                   AAM70625 standard; Protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM58174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-483446/52
                                                                                                                                                                      bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                         σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMTFKDY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                      marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0233687.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                   expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30279; 650pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe encoded protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schizophrenia,
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Query Match
Best Local Similarity
Matches 7; Conserv
                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                             AAM18471;
                                                                                                                                                                                                                                             AAM18471 standard;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analyzing dene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                09-AUG-2001
                                                                                                                               WO200157278-A2
                                                                                                                                                                  cervical
                                                                                                                                                                        Probe; human; microarray;
                                                                                                                                                                                           Peptide #4905
                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                               30-JAN-2001; 2001WO-US00670
                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                        138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC.
                                                                                                                                                                 cancer
                                                                                                                                                                                                                                                                                       IMTFKDY 12
                                                                                                                                                                                                                                                                                                        IMTFKDY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                         54 AA;
                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00668
                                                                                                                                                                                        encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ľ,
                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                   30931;
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                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                           for
                                                                                                                                                                                                                                             Ä
                                                                                                                                                                         expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                        measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone marrow
                                                                                                                                                                                                                                                                                                                             DB
23;
                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                        cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                       Length 54
                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                       0;
QY
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-JUC-2000;
14-JUC-2000;
14-JUC-2000;
                                                                                            19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                             02-MAR-2000;
16-MAR-2000;
                                                                                                                                              04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                17-JAN-2001; 2001WO-US01354
                                                                                                             18-APR-2000;
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밁 QY

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Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                                                                                                                                                 (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                              Sequence
                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27;
                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG,
138 IMTFKDY 144
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                              54
                                             Conservative
                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           ID No 23297; 487pp; English.
                                                             3.5%;
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                                             0.
                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    to human single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                             Mismatches
                                                                 . DB 2
                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelial cells
                                             0
                                                                                 Length
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                    acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - for
                                           0,
                                           Gaps
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cytostatic;
                                          Human immune/haematopoietic antigen SEQ ID NO:17930.
                                                                        07-NOV-2001
                                                                                                                                  AAM90337
                                                                                                                                                                                                       σ
                immune;
                                                                                                                                  standard;
                                                                                                                                                                                                       IMTFKDY 12
   gene
                                                                        (first
               haematopoietic; immune/haematopoietic antigen;
therapy; vaccine;
                                                                                                                                 Protein;
                                                                                                                                  57
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2000US-0214886. 2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0217896. 2000US-0220963. 2000US-0220964.

2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0205515.

2000US-0180628 2000US-0184664

2000US-0225213 2000US-0225214

Since

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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000
17-NOV-2000
11-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                    Claim 11; SEQ
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483426/52.
N-PSDB; AAK63118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN
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17-NOV-2000;
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17-NOV-2000;
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2000US-0249211
2000US-0249211
2000US-0249213
2000US-0249213
2000US-0249213
2000US-0249215
2000US-0249216
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2000US-0246611.
2000US-0246613.
2000US-0249207.
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2000US-0246532.
2000US-0246609.
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2000US-0246524.
2000US-0246525.
2000US-0246526.
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                                                                                                                                                                                                                                                                  NO 17930; 3071pp +
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                                                                                                                                                                                                                                                                                                               human immune/hematopoietic diagnosing and/or treating
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S
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                 Listing; English.
                                                                                                                                                                                                                                                                                                                cancers
                                                                                                                                                                                                                                                                                                                polypeptides, and
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L4-SEP-2000;

2000US-0233064

000US-0232400 000US-0232401

0000S-0232081 0000S-0231968 000**0S-**0232080

000US-0233065

14-AUG-2000 14-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000

2000US-0229344 2000US-0229343

2000US-0230438. 2000US-0231242. 2000US-0231243.

000US-0230437

000US-0231413

2000US-0226868 2000US-0227182 2000US-0226681

000US-0225759 000US-0225758 000US-0225447

2000US-0227009

14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
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02-OCT-2000
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03-OCT

2000US-0237040. 2000US-0239935. 2000US-0239937.

000US-0240960

and

2000US-0236802. 2000US-0237037. 2000US-0237038. 2000US-0237038 2000US-0237039

000US-0236369 000US-0236370 000US-0236368 000US-0236367 000US-0235836 000US-0236327

2000US-0235484 2000US-0235834

000US-0234997 000US-0234998

2000US-0241786. 2000US-0241787. 2000US-0241808. 2000US-0241806. 2000US-024481. 2000US-0244617. 2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246477.

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RESULT 13

AAM82669

ID 82669

ID 82669

ID 82669

AC AAM82

XX AM82

AC AAM82

AC AAM82

AC Human

KW Cytos

XX Cytos

XX Homo

XX Homo

XX Homo

XX Homo

XX 17-J2

PR 31-J3

PR 11-J1

PR 18-AE

PR 19-MA

PR 11-J1

PR 11-J1

PR 11-J1

PR 11-AE

PR 11-AE

PR 11-AE

PR 11-AE

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PR 31-AE

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Best Local S
Matches 7
     22-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
30-AUG-2000)
01-SEP-2000)
01-SEP-2000)
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
                                                                                                                                    14 - AUG
14 - AUG
14 - AUG
14 - AUG
18 - AUG
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000;
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      2000US-0179065
2000US-0180628
2000US-0186350
2000US-0189874
2000US-0199076
2000US-0205515
2000US-0214886
2000US-0214886
2000US-0214886
2000US-0214886
2000US-0214880
2000US-0217487
2000US-0217487
2000US-0217496
2000US-022963
2000US-0225964
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2000US-022521
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Pred. No. 24;
0; Mismatches
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29-SEP-2000;
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12-SEP-2000;
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2000US-0249207.
2000US-0249208.
2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249212.
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2000US-0246532.
2000US-0246609.
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2000US-0236370.
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2000US-0237037.
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2000US-0231414
2000US-0232080
2000US-0232081
2000US-0232081
2000US-0232397
2000US-0232398
2000US-0232399
2000US-0232401
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2000US-0229509
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RESULT 14
AAW54390
ID AAW5
XX
AC AAW5
XX
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Best Local Si
Matches 7;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 10262; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing, metastasis -
             AAW54390;
                                       AAW54390 standard; Protein;
                                                                                                                                                                                                              Sequence
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DB; AAK55450.
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8
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2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0249216
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2001US-0259678
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2000US-0251869
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                                         114 AA
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Pred. No. 32;
0; Mismatches
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D. 32;
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RESULT 15
AAU31332
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Best Local Similarity
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В
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                                                                                                                                   Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV26609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-207391/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multienzyme; infection; fungi; yeast; gram-positive bacteria; virus; dihydrobenzo(a)naphthacenequinone aglycon; antibiotic; pradimicin.
                                                                                                                                                                                                                                                AAU31332 standard; Protein; 131 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pradimicin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1996;
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          18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
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                                           16-APR-2001; 2001WO-US08656
                                                                  25-OCT-2001
                                                                                                             Homo sapiens.
                                                                                                                                                                               Novel
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                                                                                                                                                                                                                                                                                                                            170 VRLSRQL 176
                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                         73
                                                                                                                                  suppression;
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                                                                                                                                                                                                                                                                                                                                                             3.5%;
                                                                                                                                                                             protein
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Pred. No.
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                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically cengineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and concerned to express them are also useful for producing the proteins. They may be used to therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in the cartilage, tendon and/or nerve tissue growth or regeneration; commune suppression and/or stimulation; as anti-inflammatory agents; and concerned to the protein of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
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Best Local
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                            125 GLRRLHR 131
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                                                                                                                                                                                                                                                                     131 AA;
                                                                                                                                                                           3.5%; Score 7; DB 22; ilarity 100.0%; Pred. No. 49; Conservative 0; Mismatches
                                                                                                                                                                           0;
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Maximum
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is derived by analysis of the total score distribution.
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         July 7, 2003, 23:43:17; Search time 24 Seconds (without alignments) 948.692 Million cell updates/sec
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1 MDSLLMNRRKFLYQ
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932
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US-09-912-697-6

US-09-912-697-8

US-09-788-657-17

US-09-788-657-17

US-09-788-657-17

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US-09-788-657-17

US-09-788-657-17

US-09-788-657-17

US-09-788-657-18

US-09-788-657-17

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US-09-788-657-1554
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US-09-966-880A-2

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US-10-156-761-10683
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 Sequence 6326, Ap
Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 18, Appl
Sequence 17, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 31, Appli
Sequence 31, Appli
Sequence 1554, Ap
Sequence 46734, Ap
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Sequence 2, Appli
Sequence 38108, A
Sequence 1639, Ap
Sequence 10683, A
Sequence 234, App
Sequence 6326, Ap
Sequence 6326, Ap
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2000	US-10-083-720A-		ω.	5
Sequence 1, Appli	US-10-		ω.	14
ū	US-09-965-528-5		ω.	13
71	US-09-975-719-		ω.	12
	us-09-916-790-		ω.	11
Sequence 4, Appli	US-09-363-9		ω •	0
4, Appli	US-10-083-7		ω.	99
ce 954,	US-09-867-		ω.	38
Sequence 136, App	US-09-148-5		ω.	37
6,	9 US-09-981-876-136	156	6 3.0	6
ce 37707	US-09-864-		ω.	ÿ,
96, A	US-09-764-8		ω.	34
9	US-09-860-6		ω.	33
Sequence 35163, A	US-09-864-7		ω.	32
Sequence 32, Appl	US-10-193-65		ω.	31
Sequence 7988, Ap	9 US-10-156-761-7988		ω.	30
	US-10-004-381-1		ω.	
Sequence 34154, A	US-09-864-761-3415		ω.	28
Sequence 34110, A	US-09-864-761-		ω.	27
	US-10-156-761-12		ω.	26
,896	US-10-083-357-96		ω.	25
G	US-09-764-877-1		ω.	24
187,	US-08-424-550B-1		<u>ن</u>	23
49	US-09-864-761-449		ω.	22
equence 2048,	US-09-867-550-204		ω.	21
Sequence 46082, A	US-09-864-761-4		ω.	20

ALIGNMENTS

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; SOFTWARE: FASTSEQ for Win
SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-880A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HONDO, TASUKU
APPLICANT: HONDO, TASUKU
APPLICANT: HONDO, TASUKU
APPLICANT: HONDO, TASUKU
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR TILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-8
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                                                                                                                                                                                                                                                                                    100.0%; Score 198; DB 9; Similarity 100.0%; Pred. No. 1.5e-183;
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                                                                                                                                                                                                    MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL
                                                                                         FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-966-880A-2
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                                                                                                                                                                                                                          APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica x-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER: 1999-03-29
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR FILING DATE: 2001-01-30
                                                                                                                          PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
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                        APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
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42; Conservative
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Hanzel, David K.
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100.0%; Pred. No. 8.7
7ative 0; Mismatches
PCT/US01/00669
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                  Query Match 3.5%; Score 7; DB:
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXT_HUMAN HIT: AA121545.1, EVALUE 1.00e-03
                                                                      ; ORGANISM: Homo sapiens US-09-925-300-1639
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US-09-925-300-1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1639, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:
                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1639
LENGTH: 222
TYPE: PRT
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Graig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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R APPLICATION NUMBER: PCT/US01/00668
R FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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DB 10;
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). 18;
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Length 222; Indels

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Gaps

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RESULT 5
US-10-156-761-10683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ISHKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                           US-09-881-752A-234
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10683, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 234, Application US/09881752A Patent No. US20020115078A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.5%;
Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10683
                                                                                                                                                                                                                                                                                                    APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078Alel Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION UNDER: US2/09/881,752A
CURRENT FILING DATE: 2001-06-15
CURRENT FILING DATE: 2001-06-15
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                                                              Matches
                                                                                                   Query Match
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
                                                                                                                                                          LENGTH: 350
TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 327
                                                  J.5%;
Local Similarity 100.0%;
es 7; Conservation
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    96 DFLRGNP 102
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Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; ; Pred. No.
                                                              0;
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                                                              Mismatches
                                                                               DB 10; Length 350;
5. 95;
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                                                            0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-174
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,526
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6326, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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SEQ ID NO 174
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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NUMBER OF SEQ ID NOS: 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Agostino, Michael J.
Steininger II, Robert J
Spaulding, Vikki
Wong, Gordon G.
                                                                                                                                                                                                                                                               OZAKI, AKIO
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SENOH, AKIHIRO
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                            YOKOI, HARUHIKO
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                                                                                                                                                                                                                                                                                   IKEDA, MASATO
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; LENGTH: 513
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6326
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                                                                                                                                                                                                                                    Sequence 6, Application US/09912697
Publication No. US20030068808A1
GENERAL INFORMATION:
APPLICANT: Nicolaides, Nicholas C
APPLICANT: Sass, Philip M
APPLICANT: Grasso, Luigi M
APPLICANT: Kline, J Bradford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
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SEQ ID NO 4
LENGTH: 932
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CURRENT FILING DATE: 2002-02-22
PRIOR PPLICATION NUMBER: PCT/US95/01035
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 09/468,024
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
                                                                 SEQ ID NO 6
                                                                                                   TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL TITLE OF INVENTION: ANTIBIOTICS FILE REFERENCE: MOR-0040 CURRENT APPLICATION NUMBER: US/09/912,697 CURRENT FILING DATE: 2001-07-25 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/210,143
PRIOR FILING DATE: 1994-03-16
PRIOR APPLICATION NUMBER: 08/187,757
PRIOR FILING DATE: 1994-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/465,769
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/294,312
PRIOR FILING DATE: 1994-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haseltine et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 78
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                                                                                   SOFTWARE: PatentIn version 3.1
TYPE: PRT
ORGANISM: Homo sapiens
                                          ENGTH: 932
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Local Similarity 100.0%; Pred. No. 2.
res 7; Conservative 0; Mismatches
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b. 1.3e+02;
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b. 2.3e+02;
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 932
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-697-8
                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 18
LENGTH: 932
TYPE: PRT
ORCANISM: Homo sapiens
US-09-750-285-18
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US-09-760-285-18
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                                                                     Query Match
Best Local S
Matches 7
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Publication No. US20030068808A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Marches 7; Conservative (
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APPLICANT: Sass, Philip M
APPLICANT: Grasso, Luigi M
APPLICANT: Kline, J Bradford
TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL
TITLE OF INVENTION: ANTIBIOTICS
FILE REFERENCE: MOR-0040
                                                                                                                                                                                                                                                      APPLICANT: Nicolaides, Nicholas C
APPLICANT: Grasso, Luigi
APPLICANT: Grasso, Luigi
APPLICANT: Sass, Philip M
TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
FILE REFERENCE: MOR-0017
CURRENT FILLING DATE: 2001-01-15
CURRENT FILLING DATE: 2001-01-15
CURRENT SOLUTION NUMBER: 05/09/760,285
CURRENT FILLING DATE: 2001-01-15
CURRENT FILLING DATE: 2001-01-15
CURRENT FILLING DATE: 2001-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/912,697
CURRENT FILING DATE: 2001-07-25
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                                170 VRLSRQL 176
882 VRLSRQL 888
                                                          3.5%; Score 7; Similarity 100.0%; Pred. No. 7; Conservative 0; Mismaro
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                                                                 DB 9; ___
No. 2.3e+02;
0;
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o. 2.3e+02;
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RESULT 13 US-09-788-657-17

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NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 932
TYPE: PRT
ORGANIZM: Homo sapiens
US-09-788-657-17
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 18; LENCTH: 932; TYPE: PRT; ORGANISM: Homo sapiens US-09-788-657-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luigi
APPLICANT: Grasso, Luigi
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: yeast
FILE REFERENCE: 01107.00097
CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,336
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 25
                  RESULT 15
US-10-213-990-27
US-10-213-990-27
Sequence 27, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09788657 Patent No. US20020123149A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Best Local Similarity
Matches 7; Conserv
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Patent No. US20020123149A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nicolaides, Nicholas
APPLICANT: Sass, Philip
APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luigi
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: yeast
FILE REFERENCE: 01107.00097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,336
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT: Bussey, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 3.5%; Score 7; DB Local Similarity 100.0%; Pred. No. 2.: 100.0%; Pred. No. 2.: 100.0%; Mismatches 7; Conservative 0; Mismatches
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ilarity 100.0%;
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Pred. No.
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b. 2.3e+02;
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; LENGTH: 944
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-27
Дb
                                οy
                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 27
                                                                       Matches
                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                              APPLICANT: ROOMEY, TETY
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT FACILION NUMBER: US/10/213,990
CURRENT FILLING DATE: 2002-08-05
CURRENT FILLING DATE: 2002-08-05
UMMBER OF SEO ID NOS: 72
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   893 ATSFSLD 899
                                    39 ATSFSLD 45
                                                                     Similarity
7; Conserve
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                                                                       Conservative
                                                                                       3.5%; Score 7; DB 9; Le 100.0%; Pred. No. 2.3e+02;
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Search completed: July 7, 2003, 23:46:08 Job time: 24 secs

	Oy 188 DIRDAF 193		Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 14;	Query Match 3.0%; Score 6; DB 2; Length 11;		US-08-591-438-20	; MOLECULE TYPE: polypeptide	; TOPOLOGY: linear	; STRANDEDNESS: single	; TYPE: amino acid	; LENGTH: 11 amino acids	; SEQUENCE CHARACTERISTICS:	; INFORMATION FOR SEQ ID NO: 20:	; TELEX: 230 901 SANS UR	; TELEFAX: (CIC) /42-4366
; COUNTRY: USA	; STATE: California	; CITY: San Francisco	; STREET: One Market Plaza, Steuart Tower, Suite 2000	; ADDRESSEE: William M. Smith	; CORRESPONDENCE ADDRESS:	; NUMBER OF SEQUENCES: 91	; TITLE OF INVENTION: Peptide Library and Screening Method	; APPLICANT: Stemmer, Willem P.C.	; APPLICANT: Miller, Jeff F.	; APPLICANT: Cull, Millard G.	; APPLICANT: Schatz, Peter J.	; GENERAL INFORMATION:	; Patent No. 5338665	; Sequence 31, Application US/07963321	US-07-963-321-31	RESULT 7

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                  RESULT 1
US-08-816-241-1
                                                                                             Sequence 1, Application US/08816241 Patent No. 5804185
                                                                  GENERAL INFORMATION:
APPLICANT: Bandman,
APPLICANT: Goli, Su
                                                                                                                                                                                        TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
   STREET: 3174 FOR CITY: Palo Alto
                           ADDRESSEE:
                                                                                                                                                                                        Ç,
                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                        Surya K.
ON: NOVEL RNA
CES: 5
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US-09-113-977C-32

US-08-687-895-3

US-08-816-241-3

US-09-1040-482-3

US-09-128-395-3

US-09-128-395-3

US-09-201-227A-17

US-09-201-227A-2

US-08-470-851-4

US-08-470-851-4

US-08-481-560-4

US-08-170-113-4

US-08-643-810A-4

PCT-US93-07646-2

US-09-452-624A-3
                                                         EDITING ENZYME
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Run

on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	J I D	Description
1	7	3.5	190	US-08-816-241-1	Sequence 1, Appli
2	7	ω. 5	190 3	0S-09-128-395-1	Sequence 1, Appli
ω	7	ω Մ	932 /	US-08-294-312B-4	Sequence 4, Appli
4	7	3.5	932 /	US-08-468-024B-4	Sequence 4, Appli
ъ	6	3.0	11 ;	2 US-08-591-438-20	Sequence 20, Appl
on.	σ	3.O	12 :	L US-07-778-233B-31	Sequence 31, Appl
7	თ	3.0	12 :	L US-07-963-321-31	Sequence 31, Appl
80	0	3.0	12 :	L US-08-290-641-31	Sequence 31, Appl
Q	6	3.0	12	L US-08-548-540-31	Sequence 31, Appl
10	O	3.0	12 :	3 US-08-599-226-31	Sequence 31, Appl
11	0	3.0	12 ,	us-09-125-098-31	Sequence 31, Appl
12	on.	ω 0	12	5 PCT-US96-09809-31	Sequence 31, Appl

APPLICATION NUMBER: US/08/816
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

US/08/816,241

TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF

PF-0239 US

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COUNTRY:

USA

Page -

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA: 2.0 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence Sequence 3, Appli 3, Appli 3, Appli 17, Appli 17, Appli 4, Appli 5, Appli 6, Appli 7, Appli 8, Appli 9, ppli Appli

RESULT 4 US-08-468-024B-4 Sequence 4, Application US/08468024B Patent No. 6416984 GENERAL INFORMATION: APPLICANT: Haseltine et al. TITLE OF INVENTION: Human DNA Mismatch Repair Proteins FILE REFERENCE: PF106P3 CURRENT APPLICATION NUMBER: US/08/468,024B	Matches 7; Conservative 0; Mismatches 0; Indels 0 Qy 170 VRLSRQL 176
	0;

Gaps

0,

Mon Jul 14 14:47:06 2003

SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/128,395

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

ZIP: 94304 COUNTRY:

COMPUTER: IBM Compatible OPERATING SYSTEM: DOS

CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES:

ADDRESSEE:

IE: Incyte Pharmaceuticals, Inc.
3174 Porter Drive

STREET: 3174 Por CITY: Palo Alto STATE: CA

CA

USA

APPLICANT: Goli, Surya K.
FITLE OF INVENTION: NOVEL RNA EDITING ENZYME

us-09-966-880a-8.olig.rai

Page

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PRIOR APPLICATION NIMBER.
              CURRENT FILING DATE:
              1995-06-06
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Вb
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                                                                                                                                                   US-08-290-641-31
                                                                                                                                                                                                                                                     TELEFAX: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
APPLICATION NUMBER: US 07/778,223
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SMith, William M.
DECTORDATION NUMBER: 30.223
                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: 56 3 1.1
                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cull, Millard G. APPLICANT: Miller, Jeff F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market I CITY: San Francisco
                                                                                Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                  LENGTH: 12 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E OF INVENTION:
                                                126 LRRLHR 131
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                                                                                  Conservative
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                                                                                                                                                                                                  peptide
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                                                                                3.0%; Score 6; DB
100.0%; Pred. No. 15
Live 0; Mismatches
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US-08-599-226-31
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                                                                                                                 Sequence 3 Patent No.
                                                                                                 GENERAL INFORMATION:
APPLICANT:
                                APPLICANT
                                                   APPLICANT
                                                                                APPLICANT:
                                                                 APPLICANT
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RESULT 9 US-08-548-540-31

Sequence 31, Application US/08548540 Patent No. 5733731 GENERAL INFORMATION:

APPLICANT APPLICANT APPLICANT

Sakorafas, Paul Schoenhaut, David Vaughan, Tristan J.

Michael

Labkovsky, Boris Mankovich, John A.

Kaymakcalan, Zehra

Hoogenboom, Hendricus R.J.M.

Salfeld,

d, Jochen G. Deborah J.

McGuinness, Brian T. Roberts, Andrew J.

1, Application US/08599226
6090382

0;

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US-08-548-540-31
                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                     MOLECULE TYPE: per IMMEDIATE SOURCE: 56 3 1.1
                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-AUG-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PAten***
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/290,641 FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
126 LRRLHR 131
                                                                                                                                                                                                                                       415-326-2422
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1995
                                          3.0%;
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                                                                                                                                                                                                                                                                                    16528J-001240US
                                          Score 6; [
                              0; Mismatches
                                              DB 1;
                                0; Indels
                                                        Length 12;
                                0
                              Gaps
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Query Match
Best Local Similarity
'atches 6; Conserve
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US-09-125-098-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-594: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1in MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COMPATIBLE
COMPUTER: IBM CC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
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LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617)227-7400
ATTORNEY/AGENT INFORMATION: JR. MAME: DeConti, Giulio A., Jr. REGISTRATION NUMBER: 31,503 REFERENCE/DOCKET NUMBER: BB1-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: DeConti, Giulio A.
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 08-FE CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                           60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617)227-5941
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/ENTION: Human Antibodies that Bind Human TNFa
SQUENCES: 37
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Mankovich, John A.
McGuinness, Brian T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             White, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schoenhaut, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakorafas, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roberts, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaymakcalan,
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internal
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                   BBI-043
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Pred. No.
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PCT-US96-09809-31
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/548,540
FILING DATE: 26-OCT-1995
APPLICATION UNMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                  IMMEDIATE SOURCE:
CLONE: 56 3 1.1
                                                                  MOLECULE TYPE:
                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                     NAME: Smith, William M. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     TOPOLOGY:
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                                                                                                   STRANDEDNESS:
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                                                                                                                  amino acid
                                                                                                                                    12 amino acids
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                                                                                     linear
                                                                peptide
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PCT/US96/09809

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-125-098-31
                                            Best Local Similarity 100 Matches 6; Conservative
                                                                                                                                                                             TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                   40 TSFSLD 45
6 TSFSLD 11
                                                                                                                                          amino acid
                                                                                                                                                    12 amino acids
                                                                                                                               linear
                                                                                                                                                                                                    (617)227-7400
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                                                                    Score 6;
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                                             0,
                                                                    Length 12;
                                             Indels
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                                             Gaps
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Sequence 31, Application PC/TUS9609809
GENERAL INFORMATION:
                                                                                                             APPLICANT: Gates,
                                                                                                                                  APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Gates, Christian M.
                                                                         CORRESPONDENCE ADDRESS:
                                                                                               NUMBER OF SEQUENCES:
                  STREET: One Market F
California
                                  One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                             Schatz, Peter J. Cull, Millard G.
                                                        William M.
                                                                                                                 Peptide Library and Screening Method
                                                           Smith
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RESULT 13
US-08-280-157A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: JOHN R. CASPERSON
REGISTRATION NUMBER: 28,198
REFERENCE/DOCKET NUMBER: FWL-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-723-6845
TELEFAX: 713-663-7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                      CLONE:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
SOFTWARE: MS WORD 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N
ORIGINAL SOURCE: SNAKE VENOM: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25 JULY 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.2 MB
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: SIN
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TITLE OF INVENTION:
                                                                                                                                                         [MMEDIATE SOURCE:
                                                                                                                                                                                                        CELL TYPE:
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Local Similarity 100.0%; Formula 100.0%; Formula 100.0%; Page 100.0%; Page 100.0%; Solution 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 100.0%; Page 
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                           TISSUE TYPE:
                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE:
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                                                                                                                                  LIBRARY:
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                                                                                                                                                       SNAKE VENOM SEQ ID
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; PAGES:
; DATE:
US-08-280-157A-1
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                                                                       Query Match
Best Local Similarity
"hehes 6; Conserv?
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; MOLECULE TYPE:
US-08-053-131-80
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US-08-053-131-80
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transg
TITLE OF INVENTION: Produc
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 18-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 17-DEC-1991 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
FILING DATE: 16-DEC-
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
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CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, Willia REGISTRATION NUMBER:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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18-MAR-1992
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16-DEC-1992
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100.0%; Pred. No.
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100.0%; Pred. No. 19
tive 0; Mismatches
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Search completed: July 7, 2003, 23:45:33 Job time: 22 secs
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FILING DATE: 20-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
ATPORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-00091
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2400
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US-08-645-641-80
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Patent No. 5719032
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MIMBER. 19 CON 1645 641
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ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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32238654321177656
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Copyright (c) 1993 - 2003 Compus
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PMS1_HUMAN
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PAZ_NAJSP
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LTUB_CHCNI
PAZ2_MICNI
PAZ2_NAJMO
PAZ2_NAJMO
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Q10542 mycobacteri
P15845 schistosoma
Q42430 limanda lim
Q92100 pleuronecte
P54277 homo sapien
Q09716 schizosacch
Q10756 naja sputat
P21792 micrurus ni
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O6923 buchnera ap
P20258 pseudechis
P00599 naja melano
P00602 naja mossam
P00603 naja mossam
P00604 naja mossam
P00605 naja nigric
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P00596
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Q32516 lycopersico
P06265 nicotiana t
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P15445
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6 naja naja k
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	Q96ya4 sulfolobus	P46859 escherichia	P35983 canine aden	P03180 epstein-bar	066547 aquifex aeo	Q9n1q9 bos taurus	P34044 dictyosteli	Q07648 saccharomyc	P00598 naja atra (P00606 bungarus mu	Q46824 escherichia	Q9hqj2 halobacteri

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RESULT 1

NU5C_CAPBA
ID U5C_C
AC 031952
AC 031952
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Best Local S
Matches 8
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InterPro; IPR001750; Oxidored_q1_C.
InterPro; IPR001516; Oxidored_q1_N.
Pfam; PF00361; Oxidored_q1; 1.
Pfam; PF00662; Oxidored_q1_N; 1.
Pfam; PF01010; Oxidored_q1_C; 1.
Oxidoreductase; NAD; Plastoquinone; C1
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Chioroplast.
Chioroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
NCBI_TaxID=33114;
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"Combining data in phylogenetic systematics: an empirical approach using three molecular data sets in the Solanaceae.";
Syst. Biol. 43:467-481(1994).
-i- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinone = NAD(+) + plastoquinon
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NADH-plastoquinone oxidoreductase chain 5, chloroplast (EC 1.6.5.3)
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01-JAN-1988 (Rel. 06, C
01-JUN-1994 (Rel. 29, I
16-OCT-2001 (Rel. 49, I
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01-NOV-1997
01-NOV-1997
STRAIN=cv. Bright Yellow 4;
Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.-Y., Sugita M.,
Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
Tohdoh N., Shimada H., Sugiura M.;
"The complete nucleotide sequence of the tobacco chloroplast genome:
its gene organization and expression.";
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InterPro: IPR002128; Oxidored_q1_C.
InterPro: IPR001516; Oxidored_q1_N.
Pfam; PF00361; Oxidored_q1; 1.
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Pfam; PF01010; oxidored_q1_C; 1.
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mitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.
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InterPro; IPR003150; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR002128; Oxidored_q1_N.
InterPro; IPR001516; Oxidored_q1_N.
InterPro; IPR001516; Oxidored_q1; 1.
InterPro; IPR00162; Oxidored_q1; 1.
InterPro; IPR00162; Oxidored_q1_N; 1.
InterPro; IPR00101; Oxidored_q1_N; 1.
InterPro; IPR00101; Oxidored_q1_N; 1.
INTERPRO; INDERPRO; I
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Maia e Silva A., Bossier P., Vilela C., Fernandes L., Soa Guerreiro P., Rodrigues-Pousada C.;

Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY FUNCTION AS A POSITIVE REGULATOR FOR MANNOSYLPHOSPHATE TRANSFERASE. IS REQUIRED TO MEDIATI MANNOSYLPHOSPHATE TRANSFER IN BOTH THE CORE AND OUTE! PORTIONS OF N-LINKED OLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                Odani T., Shimma Y.-I., Tanaka A., Jigami Y.; "Cloning and analysis of the MNN4 gene required for phosphorylation of N-linked oligosaccharides in Saccharomyces cerevisiae."; Glycobiology 6:805-810(1996).
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"Ninety extra nucleotide in mdhr gene of tobacco chloroplast DNA: a summary of revisions to the 1986 genome sequence.";
Plant Mol. Biol. 22:1191-1193(1993).
-i- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNN4 OR YKL200C/YKL201C.

MNN4 OR YKL200C/YKL201C.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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01-JUN-1994 (Rel. 29, Created)
15-DEC-1996 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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NCBI_TaxID=4932;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MARR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                            Hypothetical protein; Transcription regulation; Complete proteome.

SEQUENCE 143 AA; 15576 MW; F9E2D590D77F00F0
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A.,
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CA_BIND 99 110
CA_BIND 135 146
SEQUENCE 154 AA; 17894 M
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                                                           042430;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 1A1 (EC 1.14.14.1) (CYPIA1).
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EMBL; M288B8; AAA29926.1;
PIR; A44977; A44977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: SM20 IS EXPRESSED IN SCH
ADULT WORMS, BUT NOT IN EGGS.
SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Parasitol. 38:211-220(1990). FUNCTION: CALCIUM-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00054; EFh;
E; PS00018; EF.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conserv
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Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith A.L., Havercroft J.C.; P-1992) to the EMBL/GenBank/DDBJ
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EF_HAND; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2325706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Platyhelminthes;
Schistosomatidae;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 3.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Membrane.
ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
EF-HAND 4 (POTENTIAL).
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Pred. No.
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20-kilodalton
                                                                                                                                                                          PRT;
Craniata;
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                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Schistosoma
                                                                                                                                                                          521
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Vertebrata;
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SCHISTOSOMULA
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 154;
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  Euteleostomi;
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MBL outstation -
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RESULT 8
CP11_PLEPL
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Matches 7
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Q92100;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and other teleosts with species specific cDNA probes: isolation and characterisation of dab cDNA and its use in expression studies with beta-naphthoflavone-treated fish.";

Comp. Biochem. Physiol. 129C:115-127(2001).

-i-FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROLDS, FATTY ACIDS, AND XENOBIOTICS.

-i-CATALYTIC ACTIVITY: RH + reduced flavoprotein + 0(2) = ROH + oxidized flavoprotein + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; 1.

PROSITE; PS00086; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Electron
Microsome; Endoplasmic reticulum.

Microsome; 463

BINDING

463

463

HEME (BY S)
MEDLINE-94251288; PubMed-8193668;
Leaver M.J., Pirrit L., George S.G.;
"Cytochrome P450 1A1 cDNA from plaice
induction of P450 1A1 mRNA in various
and isosafrole.";
                                                                                                                                                     Pleuronectes platessa (Plaice).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                    Cytochrome CYP1A1.
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                                                                                                               Pleuronectoidei;
NCBI_TaxID=8262;
                                                                                                                             Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ001724;
HSSP; P00179; 1I
                                                                        PISSUE=Liver;
                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001128; Cytochrome_P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           123
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           PEGLRRL
                                                                                                                                                                                                                8 (Rel. 37, Created)
8 (Rel. 37, Last sequence up
8 (Rel. 37, Last annotation
P450 1A1 (EC 1.14.14.1) (C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       llarity 100.
Conservative
                                                                                     N.A.
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                                                                                                                                                                                                                                                                                         STANDARD;
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Pred.
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HEME (BY SIMILARITY)
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No.
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ion update)
(CYPIA1).
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19;
             (Pleuronectes platessa) and tissues by 3-methylcholanthrene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>بــ</u>
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                                                                                                                                                                          Euteleostomi;
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Best Local S
Matches 7
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P54277;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                       'MS1 PMSL1.

Homo sapiens (Human).

Homo sapiens (Homan; Chordata;

'horvota; Metazoa; Chordata;

horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase; Electron transport; Membrane; Microsome; Endoplasmic reticulum.
BINDING 463 HERE (BY SIMILARITY).
SEQUENCE 521 AA; 59061 MW; AA7A97CB4578F9E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X73631; CAA52010.1; -.
HSSP; P00179; LDT6.
InterPro; IPR001128; Cytochrome_P450
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF STRUCTURALLY UNRELATED MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FAITY ACIDS, AND XENOBIOTICS.
-!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)0.
-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-!- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC) AND ISOSAFROLE (ISF).
                                                                                                                                                                                               TISSUE-Gall bladder;

MEDLINE-94352394; PubMed-8072530;

MEDLINE-94352394; PubMed-8072530;

Nicolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K. Micolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K. Micolaides N.C., Papadopoulos N., Fleischmann R.D., Ruben S.M., Rosen C.A., Hamilton S., Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S., Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.;

"Mutations of two PMS homologues in hereditary nonpolyposis co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                             cancer.";
                                                                                                          Wang
                                                                                                                                                      Nature 371:75-80(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 PMS1 protein h
                                               hMSH6 genes
                                                                              Pulsieux A.,
                                                                                            Navarro C.,
                                                                                                                        MEDLINE=99408236;
                                                                                                                                          VARIANTS
                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00086; CYTOCHROME_P450;
                                                             "Prevalence
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event Buropean Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
   FUNCTION:
                                                                                                       Q., Lasset C.,
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(Rel. 34, Last sequence up
(Rel. 41, Last annotation
                                               p of
                  105:79-85(1999)
                                                                                            Ruano E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   PROBABLY
                                               germline mutations of hMLH1, hMSH2, 1
75 French kindreds with nonpolyposis
                                                                                                                                      THR-394 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                         R-394 AND ARG-501.
PubMed=10480359;
... Desseigne F., Saurin J.-C.,
E., Descos L., Trillet-Lenoir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                1 (DNA mismatch repair protein PMS1).
INVOLVED IN
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   THE REPAIR OF MISMATCHES IN
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                                                                                                                                                                                                  hereditary nonpolyposis colon
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                                                                                          Maugard
V., Boss
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                                                              hPMS1, hPMS2,
                                                                                                                                                                                                                                                R.D.,
                                                colorectal
                                                                                            Bosset J.-F.,
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RESULT 10
YA3B_SCHPO
ID YA3B_SCHPO

STANDARD

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Matches 7
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                                                                                                                                                      InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair.
InterPro; IPR0020910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                        EMBL; U13695; AAA
HSSP; P23367; 1BKI
Genew; HGNC:9121;
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               -
                                                                             VARIANT
                                                                                              DNA repair; Anti-oncogene; Nuclear protein;
Hereditary nonpolyposis colorectal cancer; Disease mutation
VARIANT 394 394 M -> T (IN INCOMPLETE HNPCC).
                                                                                                                                    SMART; SM00398; HMG; 1.
TIGRFAMS; TIGR00585; mutl; 1.
                                                                                                                                                                                                                MIM; 600258;
                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear (Potential).

DISEASE: ASSOCIATED WITH FAMILIAL HEREDITARY NONPOLYPOSIS COLON
PROPRESSION OF THE MOST COMMON
                                                                                                                                                                                                                                                                                                                                           DATABASE: NAME=Hereditary non-polyposis colorectal cancer www="http://www.nfdht.nl/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANCER (HNPCC) (I
GENETIC DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLON CANCERS
                    Similarity 7; Conser
 VRLSRQL 176
                                                                                                                            PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                           932
                                                                              501
                  Conservative (
                                                                                                                                                                                                                                             AAA63922.1; -.
                                                                                                                                                                                                                                    1BKN
                                                           AA;
                                                                                                                                                                                                                          PMS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LYNCH SYNDROME). HNPCC IS (
                                                                              501
                                                           105830 MW;
                                         3,58;
                     0,
                             Score 7;
Pred. No
                                                                            /FTId=VAR_012967.
G -> R (IN INCOMPLETE HNPCC)
                                                           /FTId=VAR_012968.
                             No.
                                        DB 1;
                      0;
                                        Length 932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCOUNTS
                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                   a collaboration
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                      0;
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                      Gaps
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RESULT 11
PA2_NAJSP
ID PA2_NAJSP
AC Q10756;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA William R., Simmonds M., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Ginmonres B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Girymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Wottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
                                                                                                            DЬ
                                                                                                                                        Qy
                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q09716;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C18B11.11 in chromosome I.
SPAC18B11.11 OR SPAC1F5.01.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a companies the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                              EMBL; 250728; CAA90595.1; EMBL; Z68136; CAA92229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                          460
                                                                                                                                             40
                                                                                                                                                                               . Similarity 7; Conserv
                                                                                                                                                                                                                                                    ical protein; Transmembrane.
205 225 POTENTIA
207 297 POTENTIA
277 297 POTENTIA
553 573 POTENTIA
553 888 908 POTENTIA
1294 AA; 149192 MW; 8245
                                                                                                                                            TSFSLDF
                                                                                                                                                                                 Conservative
                  STANDARD;
                                                                                                                                             46
                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                    3.5%;
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                                                                                                                                                                                              Score 7;
Pred. No
                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
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W; 82457B940A047469 CRC64;
                  PRT;
                                                                                                                                                                               mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                  DB 1
                  16
                                                                                                                                                                               0
                                                                                                                                                                                                                  Length 1294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                               0;
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolas
(Muscarinic inhibitor) (Fragment).
Naja sputatrix (Malayan spitting cobra).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                             P21790;
O1-MAY-1991 (Rel. 18, Created)
O1-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 isozyme 1 (EC 3.1.1.4) (Phosphatidylcholine
2-acylhydrolase) (Fragment).
           Mochca-Morales J., Martin B.M., Zamudio F.Z., Possani L.D.;
"Isolation and characterization of three toxic phospholipases from
the venom of the coral snake Micrurus nigrocinctus.";
Toxicon 28:616-617(199).

-!- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF TH
ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES. INHIBITS NEUROMUSCULAR
TRANSMISSION BY BLOCKING ACETYLCHOLINE RELEASE FROM THE NERVE
TERMINI. ACT PRESYNAPTICALLY.
                                                                                                                                                                                                                     Micrurus nigrocinctus (Central American coral snake) (Gargantilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                   MICNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presynaptic neurotoxin; Postsynaptic neurotoxin.
NON_TER 16 16
SEQUENCE 16 AA; 1969 MW; 9AC1F9834BB585F0 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00068; phoslip; 1.
PROSITE; PS00118; PA2_HIS;
PROSITE; PS00119; PA2_ASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acetylcholine receptor inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elapidae; Elapinae; Naja.
NCBI_TaxID=33626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Phospholipase A2 from Naja naja sputatrix venom is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96195757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                        Elapidae; Elapinae;
                                                                                                                                                                                                                                                                                                                                                                   PA21_MICNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00119; PA2_ASP; PARTIAL.
Hydrolase; Lipid degradation; Calcium; Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00598; 1POA.
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                         NCBI_TaxID=8635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h. Biochem. Biophys. 328:17-25(1996).
FUNCTION: PA2 CATALYZES THE CALCIUM DEPENDENT
ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES. BLOCKS
TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TACETYLCHOLINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.
COFACTOR: Binds 1 calcium ion per subunit (By simila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYOFKN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001211; PhospholipaseA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.0%; Sillarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed-8638927;
                                                                                                                                                                                                        Micrurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 6;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                red. No. 9.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                    27
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ВВ
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8 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLYSIS OF THE NEUROMUSCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
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CATALYTIC

Phosphatidylcholine

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                                                                                                                                 Query Match
Best Local :
                                                                                                           Matches
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PA23_MICNI STANDARD; PR
PA1792;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sneque
15-UUN-2002 (Rel. 41, Last sneque
Phospholipase A2 isozyme 3 (EC 3
2-acylhydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEQUENCE.

JISSUE-Venom;

Mochca-Morales J., Martin B.M., Zamudio F.Z., Possanı L...,

Mochca-Morales J., Martin B.M., Zamudio F.Z., Possanı L...,

Mochca-Morales J., Martin B.M., Zamudio F.Z., Possanı L...,

"Issulation and characterization of three toxic phospholipases from

the venom of the coral snake Micrurus nigrocinctus.";

Toxicon 28:616-617(1990).

TOXICON 28:616-617(1990).

TOXICON PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE

-1- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT NEUROMUSCULAR

TOXICON PAZ CATALYZES THE CALCIUM-DEPENDENT NEUROMUSCULAR

TOXICON PAZ CATALYZES THE CALCIUM-DEPENDENT NEUROMUSCULAR

TOXICON PAZ CATALYZES THE CALCIUM-DEPENDENT NEUROMUSCULAR

TOXICON PAZ CATALYZES THE CALCIUM RELEASE FROM THE NERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micrurus nigrocinctus (Central American coral snake) (Gargantilla Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapidae; Micrurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001211; PhospholipaseA2. Pfam; PF00068; phoslip; 1.
PROSITE; PS00118; PA2_HIS; PARTIAL. PROSITE; PS00119; PA2_ASP; PARTIAL. PROSITE; PS00119; PA2_ASP; PARTIAL. Hydrolase; Lipid degradation; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds I calcium ion per subunit (By s
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAM
PIR; A35948; A35948.
HSSP; P00598; 1PQA.
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00068; phoslip; 1. ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                          Multigene family.
                                                                                                                                                                                                                                                                                         PROSITE; PS00118; PA2_HIS; PARTIAL.
PROSITE; PS00119; PA2_ASP; PARTIAL.
Hydrolase; Lipid degradation; Calcium; Presynaptic neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001211; PhospholipaseA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; C35948; C35948.
HSSP; P15445; 1A3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Gisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamet Medical Rase";
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99206606; PubMed=10192388; Kalman S., MitChell W., Marathe R., Lammel C., Fe Colinger L., Grimwood J., Davis R.W., Stephens R.S. "Comparative genomes of Chlamydia pneumoniae and "Comparative genomes of Chlamydia pneumoniae and nat. Genet. 21:385-389(1999).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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16-OCT-2001 (Rel. 40, Last sequence u.
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                AE001618; AAD18482.1;
AE002203; AAF38268.1;
AP002546; BAA98543.1;
CP0425; -.
  35 NRRKFL
                                                                                             Similarity 6; Conserv
                                             NRRKFL 12
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-I SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1 OMEGA CHAIN (BY SIMILARITY).

-I DOMAIN: THE AMING-TERMINAL PORTION IS INVOLVED IN THE ASSEMBLY OF CORE RNAP, WHEREAS THE C-TERMINAL IS INVOLVED IN INTERACTION WITH TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001700; RNA_pol_A_bac.
Pfam; PF01000; RNA_pol_A_bac; 1.
ProDom; PD001179; RNA_pol_A_bac; 1.
Transcription; DNA-directed RNA polymerase.
NON_TER 13 113
SEQUENCE 113 AA; 12415 MW; 033FD3361D5E8F2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            four ribosomal RNA proteins, initiation factor-3, and the alpha subunit of RNA polymerase.";
Curr. Microbiol. 24:23-29(1992).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID-98794;
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16-0CT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (Transcriptase
alpha chain) (RNA polymerase alpha subunit) (Fragment).
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-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                        A;Status: preliminary
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ALIGNMENTS

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hypothetical protein all7084 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC712 C.Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Jate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C.Accession: AD2488
R: Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2488
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13805
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A;Introns: 862/1; 915/3; 1003/1; 1080/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Barrio, R.; Shea, M.J.; Carulli, J.; Lipkow, K.; Gaul, U.; Frommer, G.; Schuh, R.; submitted to the EMBL Data Library, August 1996
A;Description: The spait-related gene of Drosophila melanogaster is a member of an an A;Reference number: 217768
                                                                                                                                                                 A; Experimental source: strain
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Best Local Similarity
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                                                                                                                                                                    GB:BA000020; PIDN:BAB78168.1; PID:g17135622; GSPDB:GN00180
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C;Accession: T12139
R;Smith, J.F.; Kresge, M.E.;
submitted to the EMBL Data L
A;Description: A cladistic a
A;Reference number: Z17428
A;Accession: T12139
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C:Superfamily: NADH dehydrogenase (ubiquinone)
C; Keywords: chloroplast; membrane-associated co
             NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain C;Species: chloroplast Briliantaisia lamium C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #C;Accession: T12648
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A; Cross-references: EMBL: AF040144;
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C:Species: chloroplast Bellonia sp. 'Ev
C:Date: 23-Jul-1999 #sequence_revision
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A; Residues: 1-685 <SMI>
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A cladistic analysis of ndhF sequence
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A;Note: the nucleotide sequence was submitte R;Suglura, M.
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                                                                                                              A; Molecule type: DNA
A; Residues: 1-740 <OLM>
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A;Molecule type: DNA
A;Residues: 1-699 <SCO>
A;Cross-references: EMBL
C;Genetics:
A;Genome: chloroplast
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C; Superfamily
C; Keywords: c
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C; Superfamily
C; Keywords: c
N;Alternate names: NADH-ubiquinone oxidoreductase chain 5; ndh5 protein C;Species: chloroplast Nicotiana tabacum (common tobacco) C:Date: 30.7un-1987 #sequence_revision 14-Aug-1998 #text_change 03-Jun-2C;Accession: S37352; A00454 R;Olmstead, R.G.; Sweere, J.A.; Wolfe, K.H. Plant Mol. Biol. 27 Sweere, J.A.; Wolfe, K.H. Alternate and State and St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Scotland, R.W.; Sweere, J.A.; Reeves, P.A.; Olmstead, R.G. submitted to the EMBL Data Library, July 1994
A;Description: Higher level systematics of Acanthaceae determined A;Reference number: Z17564
A;Accession: T12648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
C;Genetics:
A;Genome: chloroplas
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A;Title: Evidence for the polyphyly of the
A;Reference number: Z17559
A;Accession: T13494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T134
R; Olmstead, R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain C;Species: chloroplast Nematanthus hirsutus C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 iC;Accession: T13494
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A; Residues: 1-705 <0
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Best Local :
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Keywords: chloroplast; membrane-associated complex;
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d. 82, 176-193,
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PIDN:AAA84685.

Data

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chloroplast DNA:

a summary

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mannosylphosphorylation protein MNN4 - yeast (Saccharomyces cerevisiae) W.Alternate names: protein YKL200c; protein YKL201c C.Species: Saccharomyces cerevisiae C.Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 19-Apr-C.Accession: S78475; S38037; S38038; R.Odani, T.; Shimma, Y.; Yoshifumi, J. submitted to the EMBL Data Library, January 1996 A.Description: Cloning and Analysis of the MNN4 Gene Required for Phospl A.Reference number: S78475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1178 <ODA>
A;Residues: 1-1178 <ODA>
A;Cross-references: EMBL:D83006; NID:g1752735; PID:d1012343; PID:g1752736; MIPS:YKL201c
A;Note: this is a revision to the sequence from reference S38024
R;Maia e Silva, A.; Bossier, P.; Vilela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; Fsubmitted to the Protein Sequence Database, March 1994
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; 1
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A;Residues: 1-578,609-691,'TD',694-740 <SUG>
A;Residues: 1-578,609-691,'TD',694-740 <SUG>
A;Experimental source: cv. Bright Yellow 4
R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, BMBO J. 5, 2043-2049, 1986
A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its @
                                                                                                                                                                                                                                                                                                                                      A, Experimental source: strain S288C A, Note: this sequence has been revised in reference S78475 A, Note: this was assumed to be the complete sequence of pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain S288C A;Note: this sequence has been revised in reference S78475 A;Note: this was assumed to be protein YKL200c A;Accession: S38038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 121-249, 'AIQLQT', 255, 'MALLRD', 262-390, 'LRISSSN', 398-515, 'LG' <MAI>A;Cross-references: EMBL: Z28200; NID: 9486355; PID: 9486356
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A; Accession: S38037
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                                                                                                                                                                   A; Description: required for phosphorylation of N-linked oligosaccharides C; Keywords: transmembrane protein
                                                                                                                                                                                                                                            A; Map position:
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A; Residues: 640-1178
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:28-44/Domain:
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hypothetical protein Rv0880 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C;Accession: E70780

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Havercroft, J.C.; Huggins, M.C.; Dunne, D.W.; Taylor, D.W. Mol. Blochem. Parasitol. 38, 211-220, 1990
A; Title: Characterisation of Sm20, a 20-kilodalton calcium-binding protein of Schisto A; Reference number: A44977; MUID:90220753; PMID:2325706
A; Accession: A44977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 13-Aug-1999 C;Accession: A44977
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C;Superfamily: tetracenomycin-biosynthetic D-ring
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A; Residues: 1-114 <DAI>
A; Cross-references: DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Dairi, T; Hamano, Y; Igarashi, Y; Furumai, T; Oki, T. Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997
A;Title: Cloning and nucleotide sequence of the putative polyketide A;Reference number: JC5850; MUID:97480928; PMID:9339544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyketide synthase (EC 2.-.-.) chain 11 - Actinomadura hibisca
C;Species: Actinomadura hibisca
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: JC5860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-90 <HAV>
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C; Species: Schistosoma mansoni
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    fluke (Schistosoma mansoni) (fragment)

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100.0%;
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100.0%; Pred. N
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RESULT 12
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A;Molecule type: DNA
A;Residues: 1-143 <COL>
A;Cross-references: GB:273101; GB:AL123456; NID:g3261565; PIDN:CAA97
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: linear chromosome C; Superfamily: regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: F98259
                                                                                                                                                                                                                                                                       transcription regulator, AsnC family lrp [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002 C;Accession: AC3025
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AC3025
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transcription regulator PA4508 [imported] - Agrobacterium tumefaciens C_\ellSpecies: Agrobacterium tumefaciens
                                  C; Genetics:
                                                                              A; Residues:
                                                                                                                                                                                                          R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-152 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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A;Reference number: A97359; PMID:11743194
A;Accession: F98259
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                                                  A; Experimental source:
                                                                A;Cross-references: GB:AE008689; PIDN:AAL44617.1;
                                                                              A; Molecule type: DNA
A; Residues: 1-152 <KUR>
                                                                                                              A;Status: preliminary
                                                                                                                                A; Reference number: A; Accession: AC3025
                                                                                                                                             A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193
                                                                                                                                                                               ster, E.W.
                                                                                                                                                                                             A; Authors: Yoo, H.; Tao,
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;;Gene:
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13;
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12;
                                                                                                                                                            Engineer Agrobacterium tumefaciens C58
                                                                                                                                                                                                                                         D.;
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D.; Kutyavin, T
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                                                                PID:g17742239; GSPDB:GN00187
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                                                                                                                                                                                                                                       T.; Levy, R.;
                                                                                                                                                                                                                                                         Wood, G.E.; Chen,
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Markelz,
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ckelz, B.
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F72665
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                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-190 <GLA>
A; Cross-references: GB:
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                                                                                                                                                            C; Superfamily:
                                                                                                                                                                                                                                                                                       A; Reference number: AB1077; A; Accession: AD1418
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A; Residues: 1-187 < KAW>
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                                                                                                                                                                                                           A; Experimental source:
                                                                                                                                                                                                                                                                       A; Status: preliminary
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A; Accession: F72665
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Science 294, 849-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, A; Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. ok, C.; Schlueter, T.; Muld. 21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                               glutamine amidotransferase homolog lmo2749 [imported] - Listeria C:Species: Listeria monocytogenes C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change C:Accession: AD1418 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein APE0749 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: F72665
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                                                                      glutamine amidotransferase;
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Dussurget, O.; Entian, K.D.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Strausberg R.;
Submitted (APR-2001) to the
EMBL; AB040431; BAB12721.1;
EMBL; AB040430; BAB12720.1;
EMBL; BC006296; AAH06296.1;
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MEDLINE=20460541; PubMed=11007475;

REVY P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O.,

Revy P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O.,

Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,

Tezcan I., Ersoy F., Kayserili H., Ugazio A.G., Brousse N.,

Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer A.,
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-20408890; PubMed-10950930;

MUTO T., Mutramattsu M., Taniwaki M., Kinoshita K., Honjo T.;

"Isolation, tissue distribution and chromosomal localization numan activation induced cytidine deaminase (hAID) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TERMBLIE1. 16, Created)
01-WAR-2001 (TERMBLIE1. 16, Last sequence update)
01-WAR-2002 (TERMBLIE1. 20, Last annotation update)
Activation-induced cytidine deaminase.
                                                                                                                                      "Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2)."; Cell 102:565-575(2000).
                                                                                      TISSUE=B-CELL;
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Matches 198
P91639 PRELIMINARY; PRT; 1263 AA. P91639; 01-MAY-1997 (TrEMBLrel. 03, Created) 01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-MAY-1997 (TrEMBLrel. 03, Last annotation update 21nc-finger protein SALR (SPALR-related protein). SALR OR CG4881.

SALR OR CG4881.

Drosophil', melanogaster (Fruit fly).

Eukaryona; Metazoa; Arthropoda; Tracheata; Hexapo
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PROSITE; F
SEQUENCE
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01-NOV-1999 (TremBLrel. 12,
01-MAR-2002 (TremBLrel. 20,
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
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198 AA; 23953 MW; 3C27BB143DB184A9
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Lang Q., Chen L.X.,
RA George R.A., Degers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Haril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Batler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Best Local :
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Interpro; IPR003006; Ig_MCC.
Interpro; IPR003006; Ig_MCC.
Interpro; IPR003006; Ig_MCC.
Interpro; IPR003006; Zf_CCH2; 8.

PRINTS; PR00048; ZINCFINEER.
SMART; SM00355; ZNF_C2H2; 8.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNCREACCH2_1; 8.

PROSITE; PS00290; IG_MHC; UNCREACCH2_2; 7.

PROSITE; PS00290; INC_FINGER_C2H2_2; 7.

PROSITE; PS0028; ZINC_FINGER_C2H2_2; 7.

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01-MAY-2000
01-MAR-2002
SALR protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrio R., Shea M.J., Carulli J., Lipk
Schuh R., Jackle H., Kafatos F.C.;
"The spalt-related gene of Drosophila
ancient gene family, defined by the ad
gene spalt.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: EMBL; Y07653; CAA68937.1; HSSP; P15822; 1BBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BERKELEY;
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NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VKH3;
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nes 9; Conserv
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LOCATION: NUCLEAR (
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13,
20,
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Last sequence update)
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Pred. No.
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., RA Mount S.M., Moy M., Mulshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Noy M., Mulshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Noy M., Mulshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Noy M., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Spier E., Spradling A.C., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O., RA Zhence 287:2185-2195(200).
  Query Match
Best Local S
Matches 8
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Best Local :
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InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR000822; Znf_C2H2.

Pfam; PF00096; Zf_C2H2; 8

SMART; SM00355; ZnF_C2H2; 8.

SMART; SM00355; ZnF_C2H2; 8.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 7.

DNA-binding; Metal-binding; Zinc-finger.

SEQUENCE 1267 AA; 139540 MW; 45101DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8YL51
Q8YL51;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
                                                                                                                                            InterPro;
Plasmid; H
                                                                                                                                                                                                                                "Complete genomic sequence of the cyanobacterium Anabaena sp. strair DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Wolk C.P., Kuritz T.,
Watanabe A., Iriguchi M., Ishikawa A., Kawatsuno i
Kishida Y., Kohara M., Matsumoto M., Matsuno i
Nakazaki N., Shimpo S., Sugimoto M., Takazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                      Yasuda M., Tabata S.;
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                                                                                                                                                                       AP003600; BAB78168.1; -.
Pro; IPR001601; Methyltransf.
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9; Conserv
h 4.0%;
Similarity 100.0%;
8; Conservative
                                                                                                              Hypothetical protein;
192 AA; 21971 MW;
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(TTEMBLrel. 20, Last sequence update)
(TTEMBLrel. 21, Last annotation update)
l protein All7084.
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Score 8; DB 1; Pred. No. 2.9
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Pred. No. 1.3
0; Mismatches
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45101DB1C0F47829 CRC64;
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                                                                                                                                                                                                                                                           filamentous nitrogen-fixing PCC 7120.";
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                             DB 16;
5. 2.9;
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ima K., Kimura T.,
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Best Local
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merkel T.J., Barros C., Stibitz S.,
"Characterization of the bygR locus of
J. Bacteriol. 180:1682-1690(1998).
EMBL; AF071567; AAC23902.1;
Interpro; IPRO01633; EAL.
Pfam: pP00563; EAL; 1.
SMART; SM00052; DUF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998
01-NOV-1998
01-JUN-2002
                                                                                   Pfam; PF00662; oxio
Chloroplast; NAD; o
NON_TER 1
NON_TER 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MS87;
01-OCT-2000
01-MAR-2001
01-DEC-2001
                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

(Graham S.W., Reeves P.A., Burns A., Olmstead R.G.;

(Graham S.W., Reeves P.A., Burns A., Olmstead R.G.;

("Long branches in the seed plants and the root of the angiosperms.";

submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

1 - CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOLEMBL; AF238055; AAF90041.2;

InterPro; IPR001750; Oxidored_q1.

InterPro; IPR001750; Oxidored_q1.

Pfam; PF00361; oxidored_q1. N.

Pfam; PF00362; oxidored_q1. N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
NADH dehydrogenase subunit F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Ranunculaceae; Hydrastis. NCBI_TaxID=13569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrastis canadensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=520;
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3 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                               apidored_q1_N; 1.
AD; Oxidoreductase;
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/ta; eudicotyledons; Ranunculales;
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Last annotation updat
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                                                              FAA3624B4155C472 CRC64;
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     DΒ
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Roels P., Smets E.;

Submitted (APR-1999) to the EMBL/GenB
-i- CATRALYTIC ACTIVITY: NADH + PLASTO
EMBL; AF060158; AAC64348.1; -
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00361; oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH dehydrogenase subunit (Fragment).
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                                                                                "Solanum phylogeny inferred from chloroplast Fourth Int. Solanaceae Conf. Proc. 0:0-0(0).
-!- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE EMBL; U47421; AAB00284.1; -.
                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum.
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InterPro; IPR001750; oxidored_q1.
InterPro; IPR001516; oxidored_q1_N.
Pfam; PP00361; oxilored_q1; 1.
Pfam; PF00662; oxidored_q1_N; 1.
                                                                                                                                                                    SEQUENCE FROM N.A.
Bohs L., Olmstead R.;
                                                                                                                                                                                                                                 NCBI_TaxID=45836;
                                                                                                                                                                                                                                                                                                                 Chloroplast
                                                                                                                                                                                                                                                                                                                                    Solanum physalifolium
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8; Conserv
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412 AA;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
ogenase subunit F (Fragment).
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larity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases. IV: NADH + PLASTOQUINOL = NAD(+) + PLASTOQUINOL
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Best Local S
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Best Local
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Q9RL01;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                               Q9TKN8;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Seeger K., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Kieser T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                             Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Gentianaceae; Exacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence operation as (2).";
coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SUBCELLULAR LOCATION: II
EMBL; ALI17385; CAB55674.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transmembrane transport protein. SC00317 or SC5G9.26C.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast; NAD; Oxidoreductase; Plastoquinone NON_TER 1 1 1 SEQUENCE 417 AA; 46556 MW; 32CA8951323F54EA
                                                      Spermatophyta; Magnoli
Asteridae; euasterids
NCBI_TaxID=13525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
SEQUENCE FROM N.A. MEDLINE=20340987;
                                                                                                                                                                                                                                                                                                               Q9TKN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2) /
                                                                                                                                                                  Exacum affine.
                                                                                                                                                                                         NDHF.
                                                                                                                                                                                                          NADH dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                  214
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 AA;
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
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    PubMed=10877943;
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BLrel. 13,
BLrel. 21,
subunit (
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antomycetaceae; Streptomyces.
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Query Match Best Local

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Best Local S
Matches
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                       "Higher level systematics of Acanthaceae determ: sequences.";
Am. J. Bot. 0.0-0(1995).
-i- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = 1
EMBL; U12660; AAA61724.1;
-InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1.C.
InterPro; IPR001516; Oxidored_q1.N.
Pfam; PF00361; oxidored_q1.C; 1.
Pfam; PF001010; oxidored_q1.C; 1.
Pfam; PF001010; oxidored_q1.N; 1.
Pfam; PF001010; oxidored_q1.N; 1.
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Mol. Phylogenet. Evol. 16:96-112(2000).

-!- CATALYTIC ACTIVITY: NADH + PLASTOQUI.
EMBL; AF147710; AAF03769.1; -.

InterPro; IPR001750; Oxidored.g1.
InterPro; IPR002128; Oxidored.g1.
InterPro; IPR001516; Oxidored.g1.
InterPro; IPR001516; Oxidored.g1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q32382;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Q9MS52;
Q9MS52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00361; oxidored_q1; 1. Pfam; PF01010; oxidored_q1_C; 1. Pfam; PF00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                            Chloroplast; NAD; Oxidoreductase; Plastoquinone NON_TER 1 1 1 1 NON_TER 646 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemigraphis alternata
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                                                   13
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Similarity 100.0%;
8; Conservative (
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8; Conserv
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521 AA;
                                                                                                                                                                                                                                            646
646 AA;
                                                                                                                                                                          Conservative
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                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sweere J.A.,
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73331 MW;
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Acanthaceae
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lato based
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1;
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on chloroplast ndhF
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                     RESULT
Q32213
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The phylogenetic relationships of Lembocarpus and (Gesneriaceae) based on ndhF sequences.";
Ann. Mo. Bot. Gard. 0:0-0(2000).
-!- CATALTYIC ACTIVITY: NADH + PLASTOQUINONE = NAI
EMBL; AF257485; AAF75262.1;
-InterPro; IPR001750; Oxidored_q1_C.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR003151; Oxidored_q1_N.
Pfam; PF00361; oxidored_q1:1.
                 Chloroplast; NAD; ONON_TER 1 1 NON_TER 675 SEQUENCE 675 AA;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
Asteridae; euasterids I; Lamiales; Gesneriaceae; Goyazia.
NCBI_TaxID=125973;
                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Acanthaceae; Eremomastax. NCBI_TaxID-37794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
NADH dehydrogenase subunit (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, La
01-DEC-2001 (TrEMBLrel. 19, La
NADH dehydrogenase (Fragment).
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                                                                                     Pfam; PF01010; oxidored_q1_C;
Pfam; PF00662; oxidored_q1_N;
                                                                                                                       Pfam; PF00361; oxidored_q1; 1.
                                                                                                                                                                                          Am. J. Bot. 0:0-0(1995).
-!- CATALYTIC ACTIVITY: NADH +
EMBL; U12659; AAA61723.1; -.
                                                                                                                                                                                                                                        sequences.";
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Chloroplast.
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                                                                                                                                       InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR001516; Oxidored_q1_N.
                                                                                                                                                                                                                                                            "Higher level systematics
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PF00662; oxidored_q1_N; 1.
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663 AA;
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                                                                       Oxidoreductase;
                     675
76873
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74858 MW;
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                     943D9622D98FA693 CRC64;
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Length 663;

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NAD(+) +

PLASTOQUINOL

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RESULT 15
Q9MUG6
Search completed: July 7, 2003, 23:44:27 Job time: 32 secs
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RS Smith J.F.;

Smith J.F.;

RY Thylogenetic resolution within the tribe Episcieae (Gesneriaceae):

RY Thylogenetic resolution within the tribe Episcieae (Gesneriaceae):

RY Tongruence of ITS and ndhF sequences from parsimony and maximum-

RY Tongruence of ITS and ndhF sequences from parsimony and maximum-

RY Tongruence of ITS and ndhF sequences from parsimony and maximum-

RY Tongruence ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.

C. -! - CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.

C. -! - CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.

REMBL; AF206197; AAF70600.1; -.

RY InterPro; IPR001786; Oxidored_q1_C.

InterPro; IPR001218; Oxidored_q1_C.

PRAM; PF00361; Oxidored_q1_N; 1.

RY Fiam; PF00361; Oxidored_q1_N; 1.

RY Fiam; PF00662; Oxidored_q1_N; 1.

RY Chloroplast; NAD; Oxidored_q1_N; 1.

RY NON_TER 684

684

684

685

SEQUENCE 684 AA; 77533 MW; 4D8B6FEA67DE6C1B CRC64;
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Q9MUG6; PRELIMINARY; PRT; 684 AA.
Q9MUG6; Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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Chloroplast.
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Title:

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Minimum DB seq
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-Q=/cgn2_l/USPT0_spcol/USS9966880/runat_07072003_142355_23030/app_query.fasta_1.391  
-Q=/cgn2_l/USPT0_spcol/USS9966880/runat_07072003_142355_23030/app_query.fasta_1.391  
-DB=\_Genneseq_101002 -CpWn_fasta_p -SUFFIX=olig.rng -MINMARCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DCCALIGN=200 -THR_SCORE=quality -THR_NIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTENT=pc -NORM-ext -HARNSIZE=500 -MINLENN=0 -MAXLENN=2000000000  
-USER-US09966880_@CGN_1_1_208_@runat_07072003_142355_23030 -NCPU=6 -ICPU=3  
-NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV_TIMEDUT=120 -WARN_TEMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=6  
-DEV_TIMEDUT=120 -WARN_TEMEOUT=30 -THREADS=1 -XGAPOP=60 -TGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
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length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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Human activation-induced cytidine deaminase encoding CDNA SEQ IJ NO: 7

Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antialergic; antialergy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Digeorge disease; AIDS; telangiectasia; common variable immunodeficiency disorder;

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             encoding activation induced cytidine deaminase, drug development for immune-related diseases inc
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immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colltis; drug allergic prininitis; Rosen disease; Digeorge disease; AIDS; ataxia telangicctasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompattbility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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Alignment
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                     The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency diseases, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, orug allergy, allergic rhinitis, Rosen immunodeficiency disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, ataxia telangiectasia, common variable immunodeficiency disease, ataxia telangiectasia, common variable immunodeficiency disease, ataxia telangiectasia, common variable
                                                                                                      II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 145-150; 174pp; Japanese
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                                                   Sequence 6564
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                                                                                       present sequence
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99JP-0178999.
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                                                                                       a genomic DNA sequence of human
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Percent Similarity:
Best Local Similarity: 5.03e-77 90.00 100.00% 100.00% 45.45% 21 Length: Matches: Conservative: 90 90 0 0

Mismatches: Indels:

US-09-966-880A-8 (1-198) x AAC55314 (1-6564)

Query Match: DB:

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133 GlyValGlnIleAlaIleMetThrPheLys

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                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                         encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic,
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                                                                                               No..
                                                                                                                                                                                                           Sequence 11204
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27-DEC-1999;
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        Similarity:
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Conservative:
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RESULT 5
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US-09-966-880A-8 (1-198) x AAC55339
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                        immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HTV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Discorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disease; major histocompatibility class II deficiency disease;
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                                                                           Nucleic acid
                                                                                                                                 Honjo
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                                                                                                      WPI;
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                                                             encoding activation induced cytidine deaminase, useful drug development for immune-related diseases including
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The present invention

describes an activation-induced

cytidine

deaminase

Claim 18; Page 150; 174pp; Japanese

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Best Local Similarity:
Query Match:
DB:
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AAC5530
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                                                                                                                                                                                                            Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatclogical; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; astima; IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IGG subclass selection disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 148
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                                                                                                                                                                               Mus musculus
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/product= "activation-induced
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05-OCT-2000

Activation induced cytidine deaminase; AID; cytidine deaminance related disease; allergy; allergic disease; antia.

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RESULT 7
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a target for
allergies -
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24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, altergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 126-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
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                                  Human activation-induced cytidine deaminase exon 4 SEQ
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CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and CC has cytidine activity similar to APOBEC-1. AID has antiallergic, CC antianaemic, antiathmatic, ophthalmological, anti-HIV and CC dermatological activities, and can be used in gene therapy. AID CC polynucleotides are useful in methods for identifying drugs for the CC treatment of B cell associated immune system disorders, immunodeficiency CC diseases and allergies, such as immunoglobulin A (IgA) deficiency CC disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic CC colitis, asthma, food allergy, drug allergy, allergic rininitis, Rosen CC disease, Digeorge disease, ataxia telangiectasia, common variable CC immunodeficiency disease, ataxia telangiectasia, common variable CC II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated CC II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated CC croding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The CC present sequence represents the exon 4 genomic DNA sequence of human AID
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HONJO
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99JP-0178999.
99JP-0371382.
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Human; immune; haematopoietic;
                                     Human immune/haematopoietic antigen genomic sequence
                                                                                    07-NOV-2001
                                                                                                                            AAK81088;
                                                                                                                                                                      AAK81088
                                                                                                                                                                   standard; DNA; 1665 BP
                                                                               (first entry)
immune/haematopoietic antigen; cancer;
                                       SEQ
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ID NO:35900

09-AUG-2001 WO200157182-A2 cytostatic; gene therapy; vaccine; metastasis;

18-APR-2000; 19-MAY-2000; 07-JUN-2000; 16-MAR-2000; 17-MAR-2000; 07-JUL-2000; 14-AUG-2000; 11-JUL-2000; 28-JUN-2000; 30-JUN-2000; 2000US-0224519 2000US-0225213 2000US-0186350 2000US-0189874 2001WO-US01354 .98123

18-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 2000US-0226279 2000US-02268681 2000US-0227182 2000US-0227182 2000US-0227009 2000US-0229343 2000US-0229344 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229345 2000US-023950 2000US-023950 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231243 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231244

2000US-0232081

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232398. 2000US-0232399. 2000US-0232400.

14-SEP-2000; 14-SEP-2000;

2000US-0233064

114-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000

2000US-0234998 2000US-0235484 2000US-0235834 2000US-0235834 2000US-0235837 2000US-0236367 2000US-0236368

2000US-0234997

13-OCT-2000; 13-OCT-2000;

2000US-0239935. 2000US-0239937.

2000US-0240960

2000US-0237038. 2000US-0237039. 2000US-0237040.

2000US-0237037 2000US-0236802. 2000US-0236369 2000US-0236370

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08-DEC-2000;
immune related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HTV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis
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                                                                                                     Activation-induced cytidine deaminase; AID;
                                                                                                                                             Human
                                                                                                                                                                                     05-FEB-2001
                                                                                                                                                                                                                             AAC55319;
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2000US-0251719.
2000US-0251479.
2000US-02514856.
2000US-0251868.
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2000US-2000US-

0246532 -0246527

)246609.)246610. 246528. S-0246524. S-0246525. S-0246526. s-0246478. s-0246523.

2000US-0246477 2000US-0246477

2000US-0244617. 2000US-0246474.

-0246475

2000US-0241809 2000US-0241787. 2000US-0241808. 2000US-0241221. 2000US-0241785.

2000US-0249218 2000US-0249244 2000US-0249245 2000US-0249245 2000US-0249264 2000US-0249265 2000US-0249299 2000US-0249299 2000US-0249299

2000US-0246613 2000US-0249207 2000US-0249207 2000US-0249208 2000US-0249210 2000US-0249211 2000US-0249211 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213

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                                              05-FEB-2001
                                                                                                                                   AAC55322
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a target for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esent invention describes an activation-induced cytidine deaminase AID structurally relates to an RNA editing enzyme APOBEC-1 and
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                                                                                                                                                                                                                   Muramatsu
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                                           (first entry)
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99JP-0178999.
99JP-0371382.
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Human activation-induced cytidine deaminase PCR primer

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NO:18

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μ,

GTAGTGAAGAGGCGTGACAGTGCTACATCC

US-09-966-880A-8 (1-198) x AAC55322

(1-30)

32 ValValLysArgArgAspSerAlaThrSer

41 30

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Query
DB:
                                                          Best Local Similarity:
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                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                             The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has anitallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID compoundation of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disease, DiGeorge disease, ataxia telangiectasia, common variable indmunodeficiency disease, AIDS (auto immunodeficiency yardorome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a specifically claimed PCR primer for human control of the AID which is also used in an example from the present invention.
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
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                                                                                                                                                                                                                                           Sequence 30
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(HONJ/) HONJO
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99JP-0178999.
99JP-0371382.
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding activation i a target for drug development for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honjo T,
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HONJO
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r immune-related diseases including
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Similarity:

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                            CC has cytidine activity similar to APOBEC-1. AID has antiallergic,
CC antianaemic, antiasthmatic, ophthalmological, anti-HIV and
CC dermatological activities, and can be used in gene therapy. AID
CC dermatological activities, and can be used in gene therapy. AID
CC polynucleotides are useful in methods for identifying drugs for the
CC treatment of B cell associated immune system disorders, immunodeficiency
CC diseases and allergies, such as immunoglobulin A (19A) deficiency
CC diseases, IgA nephritis, gamma-globulinaemia, atopic dermatitis, Rosen
CC colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
CC disease, DiGeorge disease, ataxia telangiectasia, common variable
CC immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
CC IgE disorder, and IgG subclass selection disorder. The DNA sequences
CC encoding AID may be used for gene therapy and the antibodies to the AID
CR protein may be used for diagnosis and treatment of these disorders. The
CC protein may be used for diagnosis and treatment of these for human
CC AID, which is also used in an example from the present invention.
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                               The present invention describes an activation-induced cytidine dea (AID) AID structurally relates to an RNA editing enzyme APOBEC-1
                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency syndrome; IgG subclass selection disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAPAN TOBACCO INC. HONJO T.
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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, aduq allergy, allergic dermatitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, ataxia telangiectasia, common variable
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                       Nucleic acid encoding activation induced cytidine deaminase, a target for drug development for immune-related diseases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                        Claim 20; Page 160; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                        Honjo T,
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                                                                                                                                                                                                                                          WPI; 200
P-PSDB;
                    The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1875) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene the AID another the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a specifically claimed PCR primer for human AID, which is also used in an example from the present invention.
                                                         (ABB57737-ABB72072)
                                                                                                                                                                    Claim 1;
                                                                                                                                                                                           New isolated nucleic genes from Drosophila interactions -
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018176-ABL30511), expressed DNA sequences (ABL018176-ABL30511), and the encoded proteins (ABB0737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 19880
                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic a genes from Drosophila interactions -
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P-PSDB; ABB64363.
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                                                                                                                               No.:
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Search completed: July 7, 2003, 23:50:07 Job time: 225 secs

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Command line parameters:

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-O_cgg2_1/USPTO_spool_VIS09966880/runat_07072003_142356_23062/app_query.fasta_1.391
-DB-Issued_Patents_NA -QFMT-fastap -SUFFIX=olig..rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MARITIX=oligo -TRAKS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_IMN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09966880_@CGN_1_1_36_@runat_07072003_142356_23062 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-09-244-752-4
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CORRESPONDENCE ADDRESS:
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                                               NAME: Sutton, Jeffre REGISTRATION NUMBER:
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equence 1029, A	equence	equence 3, Appl	equence 1, Appl	equence 1, Appl	equence 3, Appl	equence 150, Ap	equence 3, Appl	equence 1, Appl	ence 13, App	equence 13, App	tent No. 551891	. 517168	tent No. 551891	tent No. 517168	equence 5, Appl	equence 1120, A	equence 6, Appl	equence 2, Appl	uence 2, Appl	equence 268, Ap	equence 254, Ap	equence 59, App	equence 1, Appl	equence 43, App	equence 1, Appl	equence 1, Appl	equence 1, Appl	equence 43, App	equence 1, Appl	nenc	equence 3, Appl	equence 3, Appl

ALIGNMENTS

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Browne, MichaelapplicanT: Murphy, Kay E.
REFERENCE/DOCKET NUMBER: 931005C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shatzman, Allan R. TITLE OF INVENTION: No. 5783181el Compounds
                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia
STATE: Pennsylvania
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Best Local Similarity:
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                 Query Match:
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                                  Best Local Similarity:
                                                 Percent Similarity:
                                                                                  Pred. No.:
                                                                                                  Alignment Scores:
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                                                                                                                                                TELLERAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1006 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 4.35
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 93,028
REFERENCE/DOCKET NUMBER: 931005C3
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
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Patent No. 57831
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkenbeard, Hele
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Pennsylvania
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-470-299-9
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P310
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO SUPERIOR OF TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-199
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TOPOLOGY: lir
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                                                                                                     1002 CTCCGACGGATCCTTCTTCCTCTA 1025
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Murphy, Kay E.
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06-JUN-1995
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Matches:
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Sequence 9, Application US/08470299 Patent No. 5783181 GENERAL INFORMATION:

APPLICANT: Browne, Michael J. APPLICANT: Murphy, Kay E. APPLICANT: Chapman, Conrad G.

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RESULT 5
US-08-735-609-4/c
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Best Local Similarity:
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REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P310
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEPHONE: 610-270-5024
TELEPAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08735609 Patent No. 5955360
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalifitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,299 FILLING DATE: 06-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                     STREET: 220 Montgomery Street,
CITY: San Francisco
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STRANDEDNESS: doub
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                 COUNTRY:
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Young, Peter R.
Shatzman, Allan R.
YENTION: No. 5783181el Compounds
EQUENCES: 21
                                                                                                 United States Of
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Matches:
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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ATTORNEY/ÄGENT INFORMATION:

NAME: IDGOLIA, DIAGE E.

REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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DESCRIPTION:
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NAME: INGOLIA, DIANG E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM
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CLASSIFICATION: 435
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                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS
NUMBER OF SEQUENCES: 15
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Amalfitano, Andrea
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STREET: 220 Montgomery Street,
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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/desc = "DNA"
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores: Pred. No.:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                MOLECULE TYPE:
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REFERENCE/OOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                              DESCRIPTION:
                                                                                                   TOPOLOGY:
                                                                                                             STRANDEDNESS:
                                                                                                                                                LENGTH:
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                               H: 34303 base pairs nucleic acid
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Kumar-Singh, Rajendra
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
VENTION: IMPROVED ADENOVIRUS VECTORS
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Query Match:
US-09-966-880A-8 (1-198) x US-09-244-752-4 (1-34303)
                                         Query Match:
                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                    Pred. No.:
                                                                                                               Alignment Scores:
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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MOLECULE TYPE:
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TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                 LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 220 Montgomery Street, Su
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                 NAME: Ingolia, Diane REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                      linear
                                                                                                                                                         other nucleic acid
/desc = "DNA"
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Conservative:
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Query Match:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
                                                                                    Sequence 4, Application US/09562919 Patent No. 6451596 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/7:
APPLICATION NUMBER: <B) I
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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          APPLICANT: Chamberlain, Jeffrey S.
Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
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220 Montgomery Street, Suite 2200
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VENTION: IMPROVED ADENOVIRUS VECTORS
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Kumar-Singh, Rajendra
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Hartigan-O'Connor, Dennis J.
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<B) FILING DATE:
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                    US-08-374-483-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                          Sequence 6, application US/08374483 Patent No. 5880102 GENERAL INFORMATION:
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TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                             APPLICANT: GEORGE, SAMUEL E. APPLICANT: BLAZING, MICHAEL A. TITLE OF INVENTION: ADENOVIRAL NUMBER OF SEQUENCES: 9
                                                                               COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                 STATE:
                                                                                                                                       CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                              10380 CGCCTATCAAGACAACTCAGGAGA 10357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: INFORMATION:
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    171 ArgLeuSerArgGlnLeuArgArg 178
                                                                                               VIRGINIA
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                     ADENOVIRAL VECTOR SYSTEM
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Matches:
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PC-DOS/MS-DOS

not relevant E: other nucleic acid

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Length: Matches: Conservative: Mismatches:

35408

Gaps: Indels: not relevant

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US-08-973-334-3/c
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Best Local Similarity:
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TELEFAX: (703) 816-4100

TELEX: 200797 NIXU UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34382 bass
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
                                                                     APPLICATION NUMBER: US 0 FILING DATE: 05-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                  SOFTWARE: Patentin Release 1.0 Version 1.30 CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 08/549,489
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 34382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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Box 457, 321 No. 6261551ristown Road
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                                                                                                                                                                                                                                                                                                                                      USA
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Fisher, Krishna J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Adenovirus and Adeno-
                                                                                                            US 08/462,014
                                                                                                                                                                                     US/08/973,334
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US-09-563-869A-3/c
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (215) 540-5818 INFORMATION FOR SEQ ID NO: 3:
                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: n
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 35408 base pai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 35408 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10205 CGCCTATCAAGACAACTCAGGAGA 10182
                                                                   TELEFAX: (215) 540-5818
TELEFAX: (215) 540-5818
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/973,334
FILING DATE: CURNOWN>
APPLICATION NUMBER: US 08/549,489
FILING DATE: 27-OCT-1995
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0 Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
Associated Virus, Cell Lines, and
Methods of Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Howson and Howson
STREET: Box 457, 321 No. 6270996ristown Road
CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/563,869A FILING DATE: 03-May-2000 CLASSIFICATION: <Unknown>
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             ENGTH: 35408 base pairs
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Wilson, James M. Fisher, Krishna J.

Guang-Ping

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Query Match:

No.:

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FILING DALL:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,014
FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNYPN013
TELECOMOUNICATION: NEORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 35408 base pairs
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US-08-549-489-3,
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   Best Local Similarity:
Query Match:
DB:
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                                                                                                                               US-08-549-489-3
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Best Local Similarity:
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                                                 Percent Similarity:
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APPLICANT: Wilson, James M
APPLICANT: Gao, Guang-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NO. 6281010el Adenovirus Gene Therapy Vehicle TITLE OF INVENTION: and Cell Line NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                         TOPOLOGY: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Box 457, 3.
CITY: Spring House
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                              not relevant
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: July 8, 2003, 00:45:48 Job time: 140 secs
                                                                                                                                         US-09-966-880A-8 (1-198) x US-08-735-609-1 (1-35935)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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San Francisco
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Amalfitano, I
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0.1igo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALICN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/1/pubpna//

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ALIGNMENTS

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RESULT 1
US-09-966-880A-7
Sequence 7, Application US/09966880A
Sequence 7, Application US/09966880A
Patent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: MUTAMATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 05501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/PP0/01918
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-03-29
NUMBER: OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 2818
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEE: CDS
LOCATION: (80)...(673)
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GENERAL INFORMATION:

APPLICANT: HODJO, TASUKU
APPLICANT: HUCLANT MUTAMACEU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: DCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
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Best Local Similarity:
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NAME/KEY: 5'UTR
LOCATION: (1)...(79)
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PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 13
ENGTH: 271
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                                                                                                      US-09-966-880A-10
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-66-24
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                                                                                                                                                             SEQ ID NO 10
LENGTH: 6564
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                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JF 11-87192 PRIOR FILING DATE: 1999-03-29
                                                                                                                    TYPE: DNA
ORGANISM: Homo
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/J000/01918
PRIOR TLING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
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US-09-966-880A-35
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
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ORGANISM: Homo
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
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             CURRENT APPLICATION NUMBER: US/09/966,880A CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: PCT/JP00/01918 PRIOR FILING DATE: 2000-03-28
                                                                                     APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDI
FILE REFERENCE: 06501-088001
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PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
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APPLICANT: Muramatsu, Masam:
TITLE OF INVENTION: NOVEL CY:
FILE REFERENCE: 06501-088001
                                                                                                                         APPLICANT: Honjo, APPLICANT: Murama
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CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
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ORGANISM: HOMO
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                               CGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCA 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGTGCAAATAGCCATCATGACCTTCAAA 8076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC 7986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muramatsu, Masamichi
VENTION: NOVEL CYTIDINE DEAMINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09966880A
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                                                                                                                                            Tasuku
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49.00
100.00%
100.00%
24.75%
                                                                                                        CYTIDINE DEAMINASE
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Conservative: Mismatches: Indels: Gaps:

0000

61

148

Length: Matches:

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APPLICANT: HONJO, TASUKU
APPLICANT: MUZAMATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (1)...(2440)
; OTHER INFORMATION: n = A,T,C
US-09-966-880A-1
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                          SEQ ID NO 14
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09966880A Patent No. US20020164743A1
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PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
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    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
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LOCATION: (1)...(92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ArgCysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 GlyCysHisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGly
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                                                                                  FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: PCT/JP00/01918
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GENERAL INFORMATION:
APPLICANT: HOnjo, Tasuku
APPLICANT: Muramatsu, Masamichi
APPLICANT: MURAMATSU, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                            RESULT 9
US-09-966-880A-18
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MUTAMATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR PLING DATE: 2000-03-28
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: J9 11-87192
PRIOR APPLICATION NUMBER: J9 11-87192
PRIOR APPLICATION NUMBER: J9 11-87192
PRIOR APPLICATION NUMBER: J9 11-87192
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                                                                                                                                                                          ; Sequence 18, Application US/09966880A; Patent No. US20020164743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: F
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2172
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 GlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeu 181
                                                                                                                                                                                                                                                                                                                                               182 ProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198
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                                                                                                                                                                                                                                                                                                    1 CCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NOS: 36 FastSEQ for Windows Version 4.0
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Matches:
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Matches:
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Indels:
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RESULT 10
US-09-966-880A-24
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Query Match:
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Best Local Similarity:
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                                                                        US-09-966-880A-8 (1-198) x US-09-966-880A-24 (1-30)
                                                                                                                                                                                                                Pred. No.:
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                                                                                                                                                                        Percent Similarity:
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PRIOR FILLING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILLING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILLING DATE: 1999-03-29
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 24
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                      SerLeuLeuMetAsnArgArgLysPheLeu 12
AGCCTCTTGATGAACCGGAGGAAGTTTCTT 30
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Matches:
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Best Local Similarity:
Query Match:
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                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-17899
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
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                                                 SOFTWARE: Fa
SEQ ID NO 28
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDI
FILE REFERENCE: 06501-088001
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 11-178999 PRIOR FILING DATE: 1999-06-24
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TYPE: DNA ORGANISM: Artificial Sequence
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o. US20020164743A1
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Matches:
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; FEATURE: ; OTHER INFORMATION: Artificially synthesized primer sequence, US-09-966-880A-28

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RESULT 14
US-09-918-995-30146
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Best Local Similarity:
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1909-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-65-24
PRIOR FILING DATE: 1999-65-24
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LENGTH: 28
TYPE: DNA
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                                                                                                                                                                                                            Sequence 30146, Application US/09918995 Publication No. US20030073623A1
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                                                   CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
       SOFTWARE: FastSEQ for Windows Version 3.0 EQ ID NO 30146
                                         NUMBER OF SEQ ID NOS: 38054
                                                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Artificially synthesized primer sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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Conservative:
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Percent Similarity:
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US-09-859-361-3
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                                                     Score:
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                                                                                     Alignment Scores:
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TYPE: DNA
                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P31202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,783
EILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,361
FILING DATE: 17-May-2001
                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID
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ZIP: 19406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version
                                                                                                                                                         LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                NAME: Baumeister, Kir
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                            TELEFAX: 610-270-5090
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Clinkenbeard, Helen
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Matches:
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Search Job ti	Дb	Qy	US-09-	DB:
Search completed: July 8, 2003, 00:47:21 Job time : 157 secs	837 CTCCGACGGATCCTTCTTCCTCTA 860	176 LeuArgArgIleLeuLeuProLeu 183	US-09-966-880A-8 (1-198) x US-09-859-361-3 (1-984)	10 Gaps:
				0

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Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Qcgn2_f/USPT0_spool/US09966880/runat_07072003_142356_23048/app_query.fasta_1.391
-Q=/cgn2_f/USPT0_spool/US09966880/runat_07072003_142356_23048/app_query.fasta_1.391
-DB=EST -QFMT=fastap -UFFIX=olig rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIX=000000000
-USER=US09966880_gCGN_1_1_1525_@runat_07072003_142356_23048 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELED=6 -DELEXT=7
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Maximum DB seq
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Perfect score:
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length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 BG686133
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 743)</pre>	Homo sapiens	human.	EST.	BG686133.1 GI:13917530	BG686133	mRNA sequence	602638412F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766234 5',	BG686133 743 bp mRNA linear EST 01-MAY-2001	

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.
Location/Qualifiers
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                          PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160
                                                                                                                                                            AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
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//Clone_lib=NIH_MGC_48"
//Lissue_type="primary B-cells from tonsils (cell line)"
//lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="POrgan: B-cells; Vector: pOTB7; Site_1: xhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8%b. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/clone="IMAGE:4766234"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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Email: segref@genoscope.cns.fr,
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                                          TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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Mammalia; Eutheria;
1 (bases 1 to 872)
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                      211
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   Location/Qualifiers
            /tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECCRI; cDNA made by Oligo-dT priming.
Directionally cloned into ECCRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                 LLCM1698 row: i column:
                                                                                                                                                                                                                              /clone="IMAGE:4853069"
/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9606"
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                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                            Homo sapiens
CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation
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 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu
                                                                         AlaTrpGluG1yLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArg11eLeu
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                                                                                                                              TTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
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ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCGACGAA(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
LIRT (Life Technologies). Note: this is a NIH_MGC
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Plate: LLCM2051 row: m column: 14
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Location/Qualifiers
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Mammalia; Eutheria; F
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5', mRNA sequence.
EQ055935
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Tissue Procurement: Lou Staudt
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National Institutes of Health, M
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr
                                                                                                                                                                                                                        MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp 20
PheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrp
                                                      TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC
                                                                         SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60
                                                                                                                              GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCAGGAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Eutheria; Primates;
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BASE COUNT	FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db RESULT 6 BG757089 LOCUS DEFINITION	Qy Qy	0y 0y	00 Db Db Db Db Db Db Db Db Db Db Db Db Db
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VERSION VERSION BF975166.1 GI:12342381 KEYWORDS SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 942) AUTHORS NATIONAL Institutes of Health, Mammalian Gene Collection (MGC) TOTILE JOURNAL Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	QY 181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPhe 193 Db 625 TTGCCCCTGTATGATGATGACTTACGAGACGCATTC 663 RESULT 7	Qy 141 PhcLysAspTyrPhcTyrCysTrpAsnThrPheValGluAspHisGluArgThrPhcLys 160	Qy 101 ASnProASnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys 120	TACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTG TACATCTCGGACTGGGACCTAGACCCTGGCCGCTACCGCGTCACCTG TrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGl	Qy 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60	Qy 1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp 20	Alignment Scores: 1.41e-173 Length: 820 Score: 193.00 Matches: 193 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 12 Gaps: 0 US-09-966-880A-8 (1-198) x BG757089 (1-820)

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Plate: LLCM1207 row: a column:
High quality sequence stop: 707.
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                                                                                         sAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLe
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                                                                       AGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCCAGACAGCTTCGGCGCATCCT
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Site_2: EccRI; CDNA made by oligo-dT priming.
Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGRG/XhoI sites elected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: Louis M. Staudt,
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/tissue_type="primary B-cells from tonsils from tonsils from the cells for constructed by cloned into EcoRiyxhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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1 (Dases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: ECORI; CDNA made by Oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BF975096.1
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                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                   quality sequence stop:
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/clone="IMAGE:4336722"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
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                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                 ocation/Qualifiers
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AUTHORS
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VERSION
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1694 row: K column: 05
High quality sequence stop: 693.
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National Institutes of Health, Mammalian
Unpublished (1999)
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602711022F1 NIH_MGC_48 Homo sapiens
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Mammalia; Eutheria;
1 (bases 1 to 693)
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                                                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; I
Eutheria; Primates; Catarrhini; Hominidae;
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BG144705 522 bp mRNA linear EST 01-FEB-1 ut73f07.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:3333637 5' similar to TR:Q9WVEO Q9WVEO ACTIVATION-INDUCED CYTIDINE DEAMINASE. ;, mRNA sequence.
                                                                                                                                                                                        nHisGluArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerAr 174
                                                                                                                                                           gThrLeu 196
                                                                                                                                                                                                                                                          CCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAG
                                                                                                                                                                                                                                                                                                                         CAAATAGCCATCATGACCTTCAAAGATTATCT-TTACTGCTGGAATACTTTTGTAGAAAA
                                                                                                                                                                                                                                                                                                                                         GlnIleAlaIleMetThrPheLysAspTyrPhe-TyrCysTrpAsnThrPheValGluAs 154
                                                                                                                                                                                                                                                                                                                                                                                                       PheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyVal 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB5; Site_1: XhoI;
Site_2: ECCRI; cDNA made by oligo-dT priming.
Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9
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RESULT 13
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BB637360
          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Unpublished (1997)
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                                                                 house mouse
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (phage-resistant)"
/note="Organ: germinal B-cell; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_mouse_NMGB_bcell"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P. Shibata.Y. Hayatsu,N. Sugahara,Y. Shibata.K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake.S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Myazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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e mouse tissues.
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Hayashizaki,Y.
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                                                         prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 100 row: C column: 8
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Class: BAC ends.
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Rat BAC End Sequences from Library
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GSS.
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Other_GSSs: CH230-100C8.TJ
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Eukaryota; Metazoa;
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
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             Chu.
Pieter au
75
             /cell_type="Brain"
/note="Vector: pTARSAC2.1; Site_1: EcoRI; Site_2: I
/note="Vector: pTARSAHSd/MCW) BAC library produced
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced
Pieter de Jong"
75 c 129 g 79 t
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                                                                                                          /clone_lib="CHORI-230 Segment
                                                                                                                           /clone="CH230-100C8"
                                                                                                                                          /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                         /organism="Rattus norvegicus"
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Gallus bursal lymphocyte
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
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Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
182 c 167 g 151 t
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